

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:50 ; Search time 53.9852 Seconds
(without alignments)
1584.263 Million cell updates/sec

Title: US-09-785-215-2

Perfect score: 4058
Sequence: 1 MLPGLALLLAAWTAFALEV.....KMGNGYENPYKFEEDMON 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_032802:*

- 1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
- 2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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- 15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
- 16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*
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- 18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
- 19: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
- 20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
- 21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
- 22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	4058	100.0	770	10	Novel amyloid prec
2	4058	100.0	770	14	Mutated APP770 exo
3	4058	100.0	770	15	AA63442
4	4058	100.0	770	19	Human APP770 prote
5	4058	100.0	770	20	Human amyloid prec
6	4058	100.0	770	22	AAE10648
7	4058	100.0	770	22	Human amyloid prot
8	4058	100.0	770	22	Human amyloid prec
9	4058	100.0	770	22	Human amyloid prec
10	4058	100.0	770	22	Human amyloid prec
11	4058	100.0	772	22	Human amyloid prec

12	4058	100.0	772	22	AAE06895	Human amyloid prec
13	4058	100.0	772	22	AAU06624	Human amyloid prec
14	4058	100.0	772	22	AAU07223	Human beta-amyloid
15	4058	100.0	772	22	AAE02602	Human amyloid prec
16	4054	99.9	770	15	AAE62505	Amyloid precursor
17	4053	99.9	770	18	AAW19500	APP770 mutant A-be
18	4053	99.9	770	18	AAW19497	APP770 mutant A-be
19	4053	99.9	770	18	AAW19485	APP770 mutant A-be
20	4053	99.9	770	18	AAW19482	APP770 mutant A-be
21	4053	99.9	770	22	AAE06913	Human amyloid prec
22	4050	99.8	770	22	AAE06912	Human amyloid prec
23	4047	99.7	770	18	AAW19506	APP770 mutant A-be
24	4047	99.7	770	18	AAW19491	APP770 mutant A-be
25	4046	99.7	770	13	AAE26340	APP770. Homo sapi
26	4046	99.7	770	18	AAW19488	APP770 mutant A-be
27	4046	99.7	770	18	AAW19503	NAP gene product A-be
28	4039	99.5	770	11	AAE05717	Beta-amyloid-relat
29	3943.5	97.2	751	12	AAE10022	Sequence encoded b
30	3943.5	97.2	751	13	AAE20328	Human beta-amyloid
31	3943.5	97.2	751	20	AAE08615	Human beta-amyloid
32	3943.5	97.2	751	20	AAE08605	Human amyloid prot
33	3943.5	97.2	751	22	AAE10649	Human amyloid prec
34	3943.5	97.2	751	22	AAE06894	Human amyloid prec
35	3943.5	97.2	751	22	AAU06623	Human amyloid prec
36	3943.5	97.2	751	22	AAE02601	Human amyloid prec
37	3943.5	97.2	753	22	AAE10651	Human amyloid prec
38	3943.5	97.2	753	22	AAE06896	Human amyloid prec
39	3943.5	97.2	753	22	AAU06625	Human beta-amyloid
40	3943.5	97.2	753	22	AAU07224	Human amyloid prec
41	3943.5	97.2	753	22	AAE02603	Human amyloid prec
42	3938.5	97.1	751	18	AAW19486	APP751 mutant A-be
43	3938.5	97.1	751	18	AAW19496	APP751 mutant A-be
44	3938.5	97.1	751	18	AAW19499	APP751 mutant A-be
45	3938.5	97.1	751	18	AAW19483	APP751 mutant A-be

ALIGNMENTS

RESULT 1
AAP94775 standard; protein; 770 AA.

AC AAP94775;

XX 05-JUL-1990 (first entry)

DE Novel amyloid precursor protein (NAP).

KW SPAP; amyloid precursor protein; dysbolism; INS76; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Active-site 289..345

FT /*tag= a

PN /*label=INS76

PD EP304013-A.

XX 22-FEB-1989.

PF 16-AUG-1988; 88EP-0113283.

XX 15-AUG-1987; 87JP-0203298.

PR 21-AUG-1987; 87JP-0207995.

PR 18-NOV-1987; 87JP-0291404.

PR 11-DEC-1987; 87JP-0313228.

PR 05-FEB-1988; 88JP-0025260.

PR 10-FEB-1988; 88JP-0029366.

PR 19-FEB-1988; 88JP-0037905.

PR 25-MAY-1988; 88JP-0125660.

XX

PA (ASAH) ASAH KASEI KOGYO.
 XX
 PI Kitaguchi N, Takahashi Y, Tokushima Y, Itoh H;
 XX
 DR WPI: 1989-055458/08.
 DR N-PSDB: AAN91049.
 XX
 PT Human senile plaque amyloid precursor protein and DNA -
 PT used for study and diagnosis of dysbolism in the central nervous
 PT system.
 PS Disclosure: ; 108bp; English.
 XX
 CC AA. sequence from 289 to 345 encodes INS76 which is claimed as a senile
 CC plaque amyloid precursor (SPAP), useful for diagnosis of dysbolism in the
 CC CNS such as senile dementia.
 XX
 SQ Sequence 770 AA:
 Query Match 100.0%; Score 4058; DB 10; Length 770;
 Best Local Similarity 100.0%; Pred. No. 4,4e-289;
 Matches 770: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGALLLLAAMTARALEVPTDGNAGLLAEPOIAFCGRLLNMHNVONGKMDSDPSGTR 60
 DB 1 MRLGALLLLAAMTARALEVPTDGNAGLLAEPOIAFCGRLLNMHNVONGKMDSDPSGTR 60
 QY 61 TCIDTRREGILQCOEYVPELQITNVANOPVTIONMCKRGKRGKCKTHPHFVIRCLVG 120
 DB 61 TCIDTRREGILQCOEYVPELQITNVANOPVTIONMCKRGKRGKCKTHPHFVIRCLVG 120
 QY 121 EFVSDALLVPDCKFLHQRMDVCEYLHMHVAKETSEKSTNLHDYGMLPCGIDKFR 180
 DB 121 EFVSDALLVPDCKFLHQRMDVCEYLHMHVAKETSEKSTNLHDYGMLPCGIDKFR 180
 QY 181 GVEFVCCPLAESDNDVSDAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
 DB 181 GVEFVCCPLAESDNDVSDAEEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
 QY 241 EADDDDDDEDGEVEEAEPEBEATERTTATTTTTTSEVEVREVSQAQATGTC 300
 DB 241 EADDDDDDEDGEVEEAEPEBEATERTTATTTTTTSEVEVREVSQAQATGTC 300
 QY 241 EADDDDDDEDGEVEEAEPEBEATERTTATTTTTTSEVEVREVSQAQATGTC 300
 DB 241 EADDDDDDEDGEVEEAEPEBEATERTTATTTTTTSEVEVREVSQAQATGTC 300
 QY 301 RAMISRWYFDVTEGKCAFFYGGCGGNRNPFTEECMAVCGSAMQSLLKTPQEPFLAD 360
 DB 301 RAMISRWYFDVTEGKCAFFYGGCGGNRNPFTEECMAVCGSAMQSLLKTPQEPFLAD 360
 QY 361 PVKLPPTAASPDVADKYLETPGDENEHAHFOKAKERLEAKHREMSQVYRMEAEARQA 420
 DB 361 PVKLPPTAASPDVADKYLETPGDENEHAHFOKAKERLEAKHREMSQVYRMEAEARQA 420
 QY 421 KMLPRADKAAVONHOEKEVSELEQEAANRQOLVETHMARVEMLDRRLALENTYTL 480
 DB 421 KMLPRADKAAVONHOEKEVSELEQEAANRQOLVETHMARVEMLDRRLALENTYTL 480
 QY 481 QAVPRPRHVFVFMKLYVAEQKDRQHTLKHFEHVMPQPKAAQIRSOVMTFLRIYER 540
 DB 481 QAVPRPRHVFVFMKLYVAEQKDRQHTLKHFEHVMPQPKAAQIRSOVMTFLRIYER 540
 QY 541 MNOSLSLTVNPAVAEIDEVDELLQKEQNTSDVLANNISPRISYNDALMPSLJET 600
 DB 541 MNOSLSLTVNPAVAEIDEVDELLQKEQNTSDVLANNISPRISYNDALMPSLJET 600
 QY 601 KTTVELLPVNGEPLDDLOPMHSFGADSVPAANTEVEPEVDARADRLGTLTPRGSGLTN 660
 DB 601 KTTVELLPVNGEPLDDLOPMHSFGADSVPAANTEVEPEVDARADRLGTLTPRGSGLTN 660
 QY 661 IITEELISEVKMADEFRRHDSGYEVHOKLVFFAEDVGSNGGAILGLVGVVATVITL 720
 DB 661 IITEELISEVKMADEFRRHDSGYEVHOKLVFFAEDVGSNGGAILGLVGVVATVITL 720
 QY 721 VMLKKQYTSIHGGVVDAAVTPEERHLKMQONGYENPTYKFFEQMON 770
 DB 721 VMLKKQYTSIHGGVVDAAVTPEERHLKMQONGYENPTYKFFEQMON 770

DB 721 VMLKKQYTSIHGGVVDAAVTPEERHLKMQONGYENPTYKFFEQMON 770

RESULT 2
 AAR41546
 ID AAR41546 standard; Protein; 770 AA.
 XX
 AC AAR41546;
 XX
 DT 15-MAR-1994 (first entry)
 XX
 DE Mutated APP770 exon 17 protein fragment.
 XX
 KW Probe: mutation; exon 17; amyloid precursor protein; APP770;
 KW substitution; progressive presenile dementia; Alzheimer's disease;
 KW cerebral haemorrhage; cerebral amyloid angiopathy; 4 KD fragment;
 KW blood vessels; brain parenchyma; assay; processing; plaque.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 692
 FT /note= "Position of mutation which causes abnormal
 FT processing of App770"

PN EP561087-A.
 XX
 PD 22-SEP-1993.
 XX
 PF 20-MAR-1992; 92EP-0400771.
 XX
 PR 20-MAR-1992; 92EP-0400771.
 XX
 PA (INNO-) INNOGENETICS NV SA.
 XX
 PI Gras P, Hendriks L, Martin J, Van Broeckhoven C;
 DR WPI: 1993-296442/38.
 XX
 DR N-PSDB: AAO48860.
 XX
 PT New mutant form of beta-amyloid polypeptide - related to
 PT development of cerebral haemorrhage and Alzheimer's disease, also
 PT corresp. nucleic acid, vectors, host cells and antibodies
 XX
 PS Disclosure: Fig 4; 21pp; English.

CC This sequence is encoded by exon 17 of the amyloid precursor protein
 CC APP770. A mutation at position 2075 of the DNA sequence, a C>G
 CC substitution, causes the substitution of Ala for Gly at codon 692.
 CC This mutation has been detected in related patients with progressive
 CC presenile dementia (Alzheimer's disease) or cerebral haemorrhage due
 CC to cerebral amyloid angiopathy. It may be responsible for the
 CC deposition of a 4 kd proteolytic fragment of APP in blood vessel
 CC walls and brain parenchyma. Probes specific for the mutation (see
 CC also AAO48858-59) can be used to assay mRNA encoding substances which
 CC cause abnormal processing of APP related to plaque formation, and to
 CC detect this specific mutation.

XX
 SQ Sequence 770 AA:
 Query Match 100.0%; Score 4058; DB 14; Length 770;
 Best Local Similarity 100.0%; Pred. No. 4,4e-289;
 Matches 770: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLGALLLLAAMTARALEVPTDGNAGLLAEPOIAFCGRLLNMHNVONGKMDSDPSGTR 60
 DB 1 MRLGALLLLAAMTARALEVPTDGNAGLLAEPOIAFCGRLLNMHNVONGKMDSDPSGTR 60
 QY 61 TCIDTRREGILQCOEYVPELQITNVANOPVTIONMCKRGKRGKCKTHPHFVIRCLVG 120
 DB 61 TCIDTRREGILQCOEYVPELQITNVANOPVTIONMCKRGKRGKCKTHPHFVIRCLVG 120
 QY 121 EFVSDALLVPDCKFLHQRMDVCEYLHMHVAKETSEKSTNLHDYGMLPCGIDKFR 180

Db	121	EPVSDALLVPKCKFLIQRNDVETLHMHITAKETCSKSTINLHDYGLLPCGIDKR	180
Qy	181	GVEFVCCPLAEESNVDSADAEEDDSDVMWGGADTDYADGSEDKVVEVAEEEEVAVEEB	240
Db	181	GVEFVCCPLAEESNVDSADAEEDDSDVMWGGADTDYADGSEDKVVEVAEEEEVAVEEB	240
Qy	241	EADDEDDEDEGEVEEAEPEYEATERTTISATTTTTTTEESVEEYVREYCSQAETGC	300
Db	241	EADDEDDEDEGEVEEAEPEYEATERTTISATTTTTTTEESVEEYVREYCSQAETGC	300
Qy	301	RAMISRWFEDVTEBKCAPEFYGGGGGRNNPDREYCAVCGSAMSGSLTKTQEPDARD	360
Db	301	RAMISRWFEDVTEBKCAPEFYGGGGGRNNPDREYCAVCGSAMSGSLTKTQEPDARD	360
Qy	361	PVKLTPTTAASPDAVDKLTETPGDENEHAHFQAKERLEAKHREMRMSQVAREWEAEARQ	420
Db	361	PVKLTPTTAASPDAVDKLTETPGDENEHAHFQAKERLEAKHREMRMSQVAREWEAEARQ	420
Qy	421	KNLPRADKRAVIQHFQEKVESLEDEAANERQOLVETMARVEAMLNDRRLALENYITAI	480
Db	421	KNLPRADKRAVIQHFQEKVESLEDEAANERQOLVETMARVEAMLNDRRLALENYITAI	480
Qy	481	QAVPRPRPHVENMLKKYVRAEOKDRQHTLKFHEVYRAYVDKKAQITSOYVTHLRVYER	540
Db	481	QAVPRPRPHVENMLKKYVRAEOKDRQHTLKFHEVYRAYVDKKAQITSOYVTHLRVYER	540
Qy	541	MNOSTILLYNPAVAEEIODEVDELQKEONYSDQVLANMISEPRISYNDALMPSLTER	600
Db	541	MNOSTILLYNPAVAEEIODEVDELQKEONYSDQVLANMISEPRISYNDALMPSLTER	600
Qy	601	KTTVELLPVNGEFSLDDLPWHSFGSDVSPANTENEVEPYDARPAADRGLTTRPGSLTN	660
Db	601	KTTVELLPVNGEFSLDDLPWHSFGSDVSPANTENEVEPYDARPAADRGLTTRPGSLTN	660
Qy	661	ITTEEISEYKMDAEFRHDSGTEVHHQKLVFPAEDVGSKKAITGLMGGVVIATVITL	720
Db	661	ITTEEISEYKMDAEFRHDSGTEVHHQKLVFPAEDVGSKKAITGLMGGVVIATVITL	720
Qy	721	VWLKKKQYTSIHGGVEYDAATPEERHLSKMOONGENENPTKYFEEDOMN	770
Db	721	VWLKKKQYTSIHGGVEYDAATPEERHLSKMOONGENENPTKYFEEDOMN	770
RESULT 3			
AAR63442			
Db	AAR63442 standard: protein: 770 AA.		
Qy	AAR63442;		
Db	AAR63442;		
Qy	30-JUN-1995 (first entry)		
Db	30-JUN-1995 (first entry)		
Qy	Amyloid protein precursor APP.		
Db	Amyloid protein precursor APP.		
Qy	Amyloid protein precursor APP; beta-amyloid protein; gelatinase A;		
Db	Amyloid protein precursor APP; beta-amyloid protein; gelatinase A;		
Qy	progelatinase A; decomposing agent; prophylaxis; Alzheimer's disease.		
Db	progelatinase A; decomposing agent; prophylaxis; Alzheimer's disease.		
Qy	Homo sapiens.		
Db	Homo sapiens.		
Qy	Key		
Db	Key		
Qy	Region		
Db	Region		
Qy	Location/Qualifiers		
Db	Location/Qualifiers		
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Db	672..711		
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Db	/note= "beta-AP 1-40 gelatinase A		
Qy	cleavage sites"		
Db	cleavage sites"		
Qy	687..689		
Db	687..689		
Qy	/label= gelatinase A		
Db	/label= gelatinase A		
Qy	701..702		
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Db	/label= gelatinase A		
Qy	EP622079-A.		
Db	EP622079-A.		
Qy	02-NOV-1994.		
Db	02-NOV-1994.		

[illegible]

QY 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFEADVGSNKAIIIGLAVGVIAIVITL 720
 DB 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFEADVGSNKAIIIGLAVGVIAIVITL 720
 QY 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMOONGENPTYKFEEDQON 770
 DB 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMOONGENPTYKFEEDQON 770

RESULT 4

AAW40130 ID AAW40130 standard; Protein: 770 AA.

XX AAW40130:

XX 03-JUN-1998 (first entry)

XX Human APP770 protein.

XX Amyloid-beta peptide; A-beta; beta-AP; senile plaque; angiopathy;
 XX brain; membrane-spanning glycoprotein; beta-amyloid precursor protein;
 XX APP770; chromosome 21; human; Alzheimer's disease; AD; amyloid filament;
 XX treatment; disease; Down's syndrome; hereditary cerebral haemorrhage.

XX Homo sapiens.

XX MO9748983-A1.

XX 24-DEC-1997.

XX 18-JUN-1997; 97MO-US10601.

XX 18-JUN-1996; 96US-0665649.

XX (ATHE-) ATHENA NEUROSCIENCES INC.

XX (BGHM) BRIGHAM & WOMEN'S HOSPITAL.

XX Ciltion M, Schenk D, Selkoe DJ, Seubert PA;

XX WPI, 1998-063287/06.

XX N-PSDB; AAV10322.

XX Identifying compounds that alter cellular production of amyloid-beta
 PT 42 fragment - in vitro or in transgenic animal models, potentially
 PT useful for treatment of Alzheimer's and other amyloid deposition
 PT diseases

XX Disclosure; Fig 10; 86pp; English.

XX This sequence represents the human beta-amyloid precursor protein
 CC APP770, which is a membrane-spanning glycoprotein encoded by a gene
 CC on the long arm of chromosome 21. A fragment of the APP protein is known
 CC as the amyloid-beta peptide (A-beta), also known as the beta-AP peptide,
 CC which forms the subunit of the amyloid filaments comprising senile
 CC (amyloid) plaques and the amyloid deposits in small cerebral and
 CC meningeal blood vessels (amyloid angiopathy). The A-beta peptide can be
 CC a 39-43 amino acid fragment. This invention provides methods of screening
 CC compounds for their ability to alter the production of the A-beta
 CC peptide, which is composed of >41 amino acids, alone, or in combination
 CC with the A-beta peptide composed of 40 amino acids or less. Such agents
 CC that reduce the production of the A-beta peptide are potentially useful
 CC for treatment of Alzheimer's disease or other diseases involving amyloid
 CC deposition such as Down's syndrome, hereditary cerebral haemorrhage with
 CC amyloidosis of Dutch type and advanced aging of the brain.

XX Sequence 770 AA:

XX Query Match 100.0%; Score 4058; DB 19; Length 770;

XX Best Local Similarity 100.0%; Pred. No. 4, 4e-289;

XX Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRILNMHMYQNGKWDSPSGTK 60

DB 1 MLPGALLLLAAWTAARALEVPTDGNAGLLAEPOIAMFCGRILNMHMYQNGKWDSPSGTK 60
 QY 61 TCIDTKGGLILOYCOEYVPELOITNVEANOPVITQNNCKRGKCKTHPHFVIRCLVG 120
 DB 61 TCIDTKGGLILOYCOEYVPELOITNVEANOPVITQNNCKRGKCKTHPHFVIRCLVG 120
 QY 121 EFVSDALLVPDKCFLLHQEMDVCEFTLHHTYAKETCSKSTLHHTYGMILPCGIDKFR 180
 DB 121 EFVSDALLVPDKCFLLHQEMDVCEFTLHHTYAKETCSKSTLHHTYGMILPCGIDKFR 180
 QY 181 GVEFVCCPLAEESDNVDSADAEDSDVMWGGADTDVADSSEDKVYVAEEEEVAEVEE 240
 DB 181 GVEFVCCPLAEESDNVDSADAEDSDVMWGGADTDVADSSEDKVYVAEEEEVAEVEE 240
 QY 241 EADDEDDEDEGEVEEAEPEYEATERTSIATTTTTTESVEEYVREYCSQEAETGPC 300
 DB 241 EADDEDDEDEGEVEEAEPEYEATERTSIATTTTTTESVEEYVREYCSQEAETGPC 300
 QY 301 RAMISRMYFVTEBCKAPFEYGGGGRNNPDREYCMAYCGSAMSSLLKTQOEPLARD 360
 DB 301 RAMISRMYFVTEBCKAPFEYGGGGRNNPDREYCMAYCGSAMSSLLKTQOEPLARD 360
 QY 361 PVKLPPTAASTPDAVDKYLETPGDENHAHFQAKERLEAKHRRMSQVAREEAEARQA 420
 DB 361 PVKLPPTAASTPDAVDKYLETPGDENHAHFQAKERLEAKHRRMSQVAREEAEARQA 420
 QY 421 KNLPRADKKAIVIOFQEVESLEQEAANERQQLVETHMARVEAMLNDRRLALENTYAL 480
 DB 421 KNLPRADKKAIVIOFQEVESLEQEAANERQQLVETHMARVEAMLNDRRLALENTYAL 480
 QY 481 QAVPPRRHVFNNLKKVVRABOKROHTLKHFEHVRVADKKAAQIRSOVWTHLRVYER 540
 DB 481 QAVPPRRHVFNNLKKVVRABOKROHTLKHFEHVRVADKKAAQIRSOVWTHLRVYER 540
 QY 541 MNOSLSILYNVPAVAEIEIODEVDELQKEQNSDVLANNIISEPRISYGDALMPSLET 600
 DB 541 MNOSLSILYNVPAVAEIEIODEVDELQKEQNSDVLANNIISEPRISYGDALMPSLET 600
 QY 601 KTVYELLPVNGEESLDDLOPMHSFGADSVPAANTEVEVEPYDARPADRGTLTRPGSLTN 660
 DB 601 KTVYELLPVNGEESLDDLOPMHSFGADSVPAANTEVEVEPYDARPADRGTLTRPGSLTN 660
 QY 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFEADVGSNKAIIIGLAVGVIAIVITL 720
 DB 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFEADVGSNKAIIIGLAVGVIAIVITL 720
 QY 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMOONGENPTYKFEEDQON 770
 DB 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMOONGENPTYKFEEDQON 770

RESULT 5

AAW97996 ID AAW97996 standard; Protein: 770 AA.

XX AAW97996:

XX 21-JUN-1999 (first entry)

XX Human amyloid precursor protein.

XX Amyloid precursor protein; APP; human; gene targeting;

XX homologous recombination; transgenic mouse; transgenic animal;

XX animal model; Alzheimer's disease.

XX Homo sapiens.

XX Key Location/Qualifiers

XX FT Domain 672..711

XX FT Domain /note="beta-amyloid domain"

XX MO9909150-A1.

QY	421	KNFKAKKAAVIOHFQFKVKSLEGEAANEQOLVETMAVEALINRRRLALENYITL	480
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Db	421	KNFKAKKAAVIOHFQFKVKSLEGEAANEQOLVETMAVEALINRRRLALENYITL	480
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Db	481	QAVPRDRHVENMLKTVRAEOKROHTLKHFEHVRAVDEKKAOLRSQVMTLRYIER	540
QY	541	MNQSLSLLYNPAVAEEIODEVDELLOEQNYSDDVLANNISPRISYGNDALMPSLTET	600
Db	541	MNQSLSLLYNPAVAEEIODEVDELLOEQNYSDDVLANNISPRISYGNDALMPSLTET	600
QY	601	KTVYELLPVNGEESLDLDLPWHSFGADSVAPANTENEVEPYDARPAADRGLTTRPGSLTN	660
Db	601	KTVYELLPVNGEESLDLDLPWHSFGADSVAPANTENEVEPYDARPAADRGLTTRPGSLTN	660
QY	661	IKTEEISEVKKDADEFRRHDSGEVHNOKLVPAEFGVSNKGAIISLWAGGVIAIVYITL	720
Db	661	IKTEEISEVKKDADEFRRHDSGEVHNOKLVPAEFGVSNKGAIISLWAGGVIAIVYITL	720
QY	721	VMLKKQYTSIHNGVVEYDAVTPREEHNLKMQONGYENPTYKFEEDOMN	770
Db	721	VMLKKQYTSIHNGVVEYDAVTPREEHNLKMQONGYENPTYKFEEDOMN	770
RESULT 6			
AAE10648			
ID	AAE10648 standard; Protein; 770 AA.		
XX	AAE10648;		
XX	10-DEC-2001 (first entry)		
XX	Human amyloid protein precursor 770 (APP770) isoform.		
XX	Human; aspartyl protease 1; Aspl; amyloid precursor protein 770; APP770		
KW	Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;		
KW	amyloid plaque; neuronal loss; proteolytic; neurotropic; neuroprotective.		
OS	Homo sapiens		

XX	22-SEP-2000; 2000GB-0023315.
XX	
FR	23-SEP-1999; 99US-0155493.
FR	23-SEP-1999; 99US-0404133.
PR	23-SEP-1999; 99WO-US20881.
PR	13-OCT-1999; 99US-0416901.
PR	06-DEC-1999; 99US-0169232.
XX	
PA	(PHAA) PHARMACIA & UPJOHN CO.
XX	
PI	Bienkowski MJ, Gurney M;
XX	
DR	WPI: 2001-444208/48.
DR	N-PSDB: AAD17897.
XX	
PT	Polypeptide comprising fragments of human aspartyl protease with
PT	amyloid precursor protein processing activity and alpha-secretase
PT	activity, for identifying modulators useful in treating Alzheimer's
PT	disease -
XX	
XX	
PS	Example 8; Page 142-144; 187pp; English.
XX	
CC	The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
CC	Asp1 proteins which lack transmembrane domain or amino terminal
CC	domain or cytoplasmic domain and retains alpha-secretase activity
CC	and amyloid protein precursor (APP) processing activity. The proteins
CC	of the invention are useful for assaying hu-Asp1 alpha-secretase

CC activity, which in turn is useful for identifying modulators of
 CC hu-Asp1 alpha-secretase activity, where modulators that increase
 CC hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
 CC disease (AD) which causes progressive dementia with consequent
 CC formation of amyloid plaques, neurofibrillary tangles, gliosis and
 CC neuronal loss. Hu-Asp1 protease substrate is useful for assaying
 CC hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
 CC the substrate under acidic conditions and determining the level of
 CC hu-Asp1 proteolytic activity. The present sequence is amyloid protein
 CC precursor 770 (APP770) isoform from human.

XX
 XX Sequence 770 AA:

Query Match 100.0%; Score 4058; DB 22; Length 770;
 Best Local Similarity 100.0%; Pred. No. 4.4e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEGLALLLAAMTARALEVPTDGNAGLLAEPOIAMECGRIMHMHNVONGKWDSPSGTK 60
 1 MLEGLALLLAAMTARALEVPTDGNAGLLAEPOIAMECGRIMHMHNVONGKWDSPSGTK 60
 DB 61 TCIDTKESILQYCOEVVPELQITNVENANOPVTIONMCKRCKCKPHFVIRCLVG 120
 61 TCIDTKESILQYCOEVVPELQITNVENANOPVTIONMCKRCKCKPHFVIRCLVG 120
 QY 121 EFVSDALIVPCKKFLHOERMDVCETHLHMTYAKETSEKSTNLHDYGMLLPGIDKFR 180
 121 EFVSDALIVPCKKFLHOERMDVCETHLHMTYAKETSEKSTNLHDYGMLLPGIDKFR 180
 DB 121 EFVSDALIVPCKKFLHOERMDVCETHLHMTYAKETSEKSTNLHDYGMLLPGIDKFR 180
 121 EFVSDALIVPCKKFLHOERMDVCETHLHMTYAKETSEKSTNLHDYGMLLPGIDKFR 180
 QY 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGADTDYADGSEDKVVEVEEVEVEE 240
 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGADTDYADGSEDKVVEVEEVEVEE 240
 DB 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGADTDYADGSEDKVVEVEEVEVEE 240
 181 GVEFVCCPLAEESDNVDSADAEEDSDVMWGADTDYADGSEDKVVEVEEVEVEE 240
 QY 241 EADDEDEDEDEDEEERPEEATEERTTSIATTTTTSVEEVYREVSDEAEFGPC 300
 241 EADDEDEDEDEEERPEEATEERTTSIATTTTTSVEEVYREVSDEAEFGPC 300
 DB 241 EADDEDEDEDEEERPEEATEERTTSIATTTTTSVEEVYREVSDEAEFGPC 300
 241 EADDEDEDEDEEERPEEATEERTTSIATTTTTSVEEVYREVSDEAEFGPC 300
 QY 301 RAMLSRMVFDYTECKCAFFYGGCGGNRNFDTEECYCAVGSAMSQSLTKTQEPILAR 360
 301 RAMLSRMVFDYTECKCAFFYGGCGGNRNFDTEECYCAVGSAMSQSLTKTQEPILAR 360
 DB 301 RAMLSRMVFDYTECKCAFFYGGCGGNRNFDTEECYCAVGSAMSQSLTKTQEPILAR 360
 301 RAMLSRMVFDYTECKCAFFYGGCGGNRNFDTEECYCAVGSAMSQSLTKTQEPILAR 360
 QY 361 PVKLTPTAASPDAVDKYLETPGDENEHAFHOKAKERLEAKHREMSQVMEAEERQA 420
 361 PVKLTPTAASPDAVDKYLETPGDENEHAFHOKAKERLEAKHREMSQVMEAEERQA 420
 DB 361 PVKLTPTAASPDAVDKYLETPGDENEHAFHOKAKERLEAKHREMSQVMEAEERQA 420
 361 PVKLTPTAASPDAVDKYLETPGDENEHAFHOKAKERLEAKHREMSQVMEAEERQA 420
 QY 421 KNLKRAKKAVIOHROEVESLEBOAANERQOLVETHMARVEAMINDRRILATENYITAL 480
 421 KNLKRAKKAVIOHROEVESLEBOAANERQOLVETHMARVEAMINDRRILATENYITAL 480
 DB 421 KNLKRAKKAVIOHROEVESLEBOAANERQOLVETHMARVEAMINDRRILATENYITAL 480
 421 KNLKRAKKAVIOHROEVESLEBOAANERQOLVETHMARVEAMINDRRILATENYITAL 480
 QY 481 QAVPRPRHVNMLKRYVRAQKROHTLKFHEHVRMVDPRKAAQIRSOVTHLRIYIER 540
 481 QAVPRPRHVNMLKRYVRAQKROHTLKFHEHVRMVDPRKAAQIRSOVTHLRIYIER 540
 DB 481 QAVPRPRHVNMLKRYVRAQKROHTLKFHEHVRMVDPRKAAQIRSOVTHLRIYIER 540
 481 QAVPRPRHVNMLKRYVRAQKROHTLKFHEHVRMVDPRKAAQIRSOVTHLRIYIER 540
 QY 541 MNOGLSLIYNPAVAEELQDEVDLQKEONYSDDVLANMISEPRISYGNALMPSLET 600
 541 MNOGLSLIYNPAVAEELQDEVDLQKEONYSDDVLANMISEPRISYGNALMPSLET 600
 DB 541 MNOGLSLIYNPAVAEELQDEVDLQKEONYSDDVLANMISEPRISYGNALMPSLET 600
 541 MNOGLSLIYNPAVAEELQDEVDLQKEONYSDDVLANMISEPRISYGNALMPSLET 600
 QY 601 KTYELLPVNGEESLDDLOPHSGADSVAPNTENEVYPVARAARGLTRRSGSLTN 660
 601 KTYELLPVNGEESLDDLOPHSGADSVAPNTENEVYPVARAARGLTRRSGSLTN 660
 DB 601 KTYELLPVNGEESLDDLOPHSGADSVAPNTENEVYPVARAARGLTRRSGSLTN 660
 601 KTYELLPVNGEESLDDLOPHSGADSVAPNTENEVYPVARAARGLTRRSGSLTN 660
 QY 661 IKTEISEVKMDAEFRHDSGEVHHOKLVFEADVGSNKGAIIIGMVGVIATVIYITL 720
 661 IKTEISEVKMDAEFRHDSGEVHHOKLVFEADVGSNKGAIIIGMVGVIATVIYITL 720
 DB 661 IKTEISEVKMDAEFRHDSGEVHHOKLVFEADVGSNKGAIIIGMVGVIATVIYITL 720
 661 IKTEISEVKMDAEFRHDSGEVHHOKLVFEADVGSNKGAIIIGMVGVIATVIYITL 720
 QY 721 VMLKKKQYTSIHGVEYDAVTPBEERHLSMGOONGENPYKFEEDOMON 770
 721 VMLKKKQYTSIHGVEYDAVTPBEERHLSMGOONGENPYKFEEDOMON 770
 DB 721 VMLKKKQYTSIHGVEYDAVTPBEERHLSMGOONGENPYKFEEDOMON 770
 721 VMLKKKQYTSIHGVEYDAVTPBEERHLSMGOONGENPYKFEEDOMON 770

RESULT 7
 ID AAE11762 standard; Protein: 770 AA.

XX
 AC AAE11762;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human amyloid precursor protein (APP).
 XX
 KW Human; neuroprotective; nootropic; immunostimulant; Alzheimer's disease;
 KW anticonvulsant; vaccine; gene therapy; Pick's disease; antidiabetic;
 KW systemic amyloidosis; maturity onset diabetes; Parkinson's disease;
 KW Huntington's disease; fronto-temporal dementia; encephalopathy; ALS;
 KW amyotrophic lateral sclerosis; amyloid precursor protein; APP.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide 1..18
 FT Protein /label= Signal_peptide
 FT Protein 19..770
 FT Protein /label= Mature_human_APP_protein
 FT Domain 18..700
 FT Domain /label= Extracellular_domain
 FT Region 672..714
 FT /note= "Abeta-42/43 core peptide"
 FT Domain 700..723
 FT /label= Transmembrane_domain
 FT Region 714..770
 FT /note= "C-100 fragment"
 FT Domain 723..770
 FT /label= Intracellular_domain
 XX
 WO200162284-A2.
 PD 30-AUG-2001.
 XX
 PF 19-FEB-2001; 2001MO-DK00113.
 XX
 PR 21-FEB-2000; 2000DK-0000265.
 PR 01-MAR-2000; 2000US-186295P.
 XX
 PA (MEBI-) M & E BIOTECH AS.
 PI Birk P, Jensen MR, Nielsen KG;
 DR N-PSDB; AAD18754.
 DR WPI: 2001-589796/66.
 PT In vivo down-regulation of amyloid protein for the treatment of
 PT Alzheimer's, comprises presenting an amyloidogenic polypeptide or its
 PT subsequence and/or at least one analogue of the amyloidogenic
 PT polypeptide to the immune system -
 XX
 PS Claim 23; Page 113-116; 120pp; English.
 XX
 The invention relates to a method for in vivo down-regulation of amyloid
 CC protein such as beta amyloid (Abeta) in an animal, including human. The
 CC method comprising presenting to the animal's immune system an
 CC immunogenically effective amount of at least one amyloidogenic protein
 CC or its subsequence and/or at least one analogue of the amyloidogenic
 CC polypeptide. The amyloidogenic protein or its subsequence, and its
 CC analogue is useful for the preparation of an immunogenic composition
 CC comprising an adjuvant for down-regulating amyloid in an animal. The
 CC also useful in the treatment, prophylaxis or amelioration of Alzheimer's
 CC disease or other diseases characterised by amyloid deposits. They are
 CC also useful in the treatment of systemic amyloidosis, maturity onset
 CC diabetes, Parkinson's disease, Huntington's disease, fronto-temporal
 CC dementia, amyotrophic lateral sclerosis (ALS), Pick's disease and
 CC prion-related transmissible spongiform encephalopathies. They are also
 CC useful for inducing production of antibodies against an amyloidogenic
 CC polypeptide. The present sequence is human amyloid precursor protein
 CC (APP).
 XX
 SQ Sequence 770 AA:

Query Match 100.0%; Score 4058; DB 22; Length 770;
 Best Local Similarity 100.0%; Pred. No. 4,4e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRILNMHMYONKMDSDPSGK 60
 DB 1 MLPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRILNMHMYONKMDSDPSGK 60
 QY 61 TCIDTKEGIIQYCOEYVPELQITNVVEANOPVTIONCKRKCKCKTHPHFVIRCLVG 120
 DB 61 TCIDTKEGIIQYCOEYVPELQITNVVEANOPVTIONCKRKCKCKTHPHFVIRCLVG 120
 QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSKSTNLHDYGMLPGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSKSTNLHDYGMLPGIDKFR 180
 QY 181 GVEFVCCPLAEESDNVDSADAEDSDVMWGADTDYADGSEDKVVEAEVEEVAEVEE 240
 DB 181 GVEFVCCPLAEESDNVDSADAEDSDVMWGADTDYADGSEDKVVEAEVEEVAEVEE 240
 QY 241 EADDEDEDDEDEVEEAEPEYBEATERTSIATTTTTTSSVEVYREVCSQAETGPC 300
 DB 241 EADDEDEDDEDEVEEAEPEYBEATERTSIATTTTTTSSVEVYREVCSQAETGPC 300
 QY 301 RAMISRYFDVTEGKCAPEFYGGCGGNRNNDTEYCMAYCGSAMOSLTKTQDEPLARD 360
 DB 301 RAMISRYFDVTEGKCAPEFYGGCGGNRNNDTEYCMAYCGSAMOSLTKTQDEPLARD 360
 QY 361 PVKLPPTAASPDAVDKYLETPGDENHAFHOKAKERLEAKHRRMSQVNRMEAEAROA 420
 DB 361 PVKLPPTAASPDAVDKYLETPGDENHAFHOKAKERLEAKHRRMSQVNRMEAEAROA 420
 QY 421 KNLPRADKAVIHFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYTAL 480
 DB 421 KNLPRADKAVIHFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENYTAL 480
 QY 481 QAVPRRRHVFNMKKYVRAQKROHTLKFHEHYRWDPRKKAQOISQVTHLRVIYER 540
 DB 481 QAVPRRRHVFNMKKYVRAQKROHTLKFHEHYRWDPRKKAQOISQVTHLRVIYER 540
 QY 541 MNOSLSLYNPAAVEEIODEVDELQEKONYSDVLANMSEPRISYGNALMPSLET 600
 DB 541 MNOSLSLYNPAAVEEIODEVDELQEKONYSDVLANMSEPRISYGNALMPSLET 600
 QY 601 KTYVELLPVNGEFSIDLQPMHSEFGADSVPAANTEVEYVDPARPADRGLTTRPGSLTN 660
 DB 601 KTYVELLPVNGEFSIDLQPMHSEFGADSVPAANTEVEYVDPARPADRGLTTRPGSLTN 660
 QY 661 IKTEEISEVKMDAFPRHDSGYEVHOKLVFFAEDVSGNKGAIITGLMGGVVIATVITL 720
 DB 661 IKTEEISEVKMDAFPRHDSGYEVHOKLVFFAEDVSGNKGAIITGLMGGVVIATVITL 720
 QY 721 VMLKKQYTSIHGVEYDAVTPBEERHLSKMOONGYENPYYKFEQMON 770
 DB 721 VMLKKQYTSIHGVEYDAVTPBEERHLSKMOONGYENPYYKFEQMON 770

RESULT 8
 ID AAE06893 standard; Protein: 770 AA.
 AC AAE06893;
 DE 23-OCT-2001 (first entry)
 XX Human amyloid precursor protein 770 (APP770) isoform.
 KW Human; aspartyl protease; beta-amyloid precursor protein 770; APP770;
 KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
 KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; nootropic;
 KW neuroprotective; antisense therapy; gene therapy; chromosome 21.

OS Homo sapiens.
 XX WO200150829-A2.
 XX 19-JUL-2001.
 XX 09-MAY-2001; 2001WO-1B00799.
 XX 09-MAY-2001; 2001WO-1B00799.
 XX PA (BIEN/) BIENKOWSKI M J.
 XX PA (GURN/) GURNEY M E.
 XX PA (HEIN/) HEINRIKSON R L.
 XX PA (PARO/) PARODI L A.
 XX PA (YANR/) YAN R.
 XX PI Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
 XX WPI: 2001-483072/52.
 XX DR N-PSDB: AAD13278.
 XX PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity
 XX Claim 8; Page 171-173; 185pp; English.
 XX PS The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
 XX CC precursor protein (APP) isoforms and their corresponding DNA molecules.
 XX CC Human aspartyl proteases can act as beta-secretase proteases useful for
 XX CC treating Alzheimer's disease. APP isoforms are useful for identifying
 XX CC modulators of amyloid-beta peptide production, for use in designing
 XX CC therapeutics for the treatment and prevention of Alzheimer's disease,
 XX CC dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis
 XX CC and neuronal loss. APP isoforms are also used in methods for identifying
 XX CC inhibitors and modulators of human Asp2 activity. The invention relates
 XX CC to a method for identifying agents that modulate the activity of human
 XX CC aspartyl protease Asp2. Amyloid-beta peptides obtained from APP are used
 XX CC as a means to screen in cellular assays for the inhibitors of beta- and
 XX CC gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in
 XX CC polymerase chain reactions (PCR). The probes are useful for detecting
 XX CC Hu-Asp nucleic acids in in vitro assays and in Northern and Southern
 XX CC blots. The present sequence is human wild-type amyloid precursor
 XX CC protein 770 (APP770) isoform. APP770 gene is localized of chromosome 21.
 XX SQ Sequence 770 AA;
 QY Query Match 100.0%; Score 4058; DB 22; Length 770;
 QY Best Local Similarity 100.0%; Pred. No. 4,4e-289;
 QY Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRILNMHMYONKMDSDPSGK 60
 DB 1 MLPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRILNMHMYONKMDSDPSGK 60
 QY 61 TCIDTKEGIIQYCOEYVPELQITNVVEANOPVTIONCKRKCKCKTHPHFVIRCLVG 120
 DB 61 TCIDTKEGIIQYCOEYVPELQITNVVEANOPVTIONCKRKCKCKTHPHFVIRCLVG 120
 QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSKSTNLHDYGMLPGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSKSTNLHDYGMLPGIDKFR 180
 QY 181 GVEFVCCPLAEESDNVDSADAEDSDVMWGADTDYADGSEDKVVEAEVEEVAEVEE 240
 DB 181 GVEFVCCPLAEESDNVDSADAEDSDVMWGADTDYADGSEDKVVEAEVEEVAEVEE 240
 QY 241 EADDEDEDDEDEVEEAEPEYBEATERTSIATTTTTTSSVEVYREVCSQAETGPC 300
 DB 241 EADDEDEDDEDEVEEAEPEYBEATERTSIATTTTTTSSVEVYREVCSQAETGPC 300
 QY 301 RAMISRYFDVTEGKCAPEFYGGCGGNRNNDTEYCMAYCGSAMOSLTKTQDEPLARD 360

Db 301 RAMISRMFYDVTGKCAPFFYGGCGGNRNPFDEEYCMVCGSAMQSILKTQOEPLARD 360
QY 361 PVKLPTTAASTPDVADKYLETPEGDENEHAFQAKERLEAKHRRMSQVWREWEAEARQA 420
Db 361 PVKLPTTAASTPDVADKYLETPEGDENEHAFQAKERLEAKHRRMSQVWREWEAEARQA 420
QY 421 KNLPRADKRAVIOHFOEKVESLEOEANERQOLVETMARVEAMLNDRRLALENTYTL 480
Db 421 KNLPRADKRAVIOHFOEKVESLEOEANERQOLVETMARVEAMLNDRRLALENTYTL 480
QY 481 QAVPRPRHVFNMLKKYVAEOKDRQHTLKHFEHVAVMDPKAAQIRSQVMTLRVIYER 540
Db 481 QAVPRPRHVFNMLKKYVAEOKDRQHTLKHFEHVAVMDPKAAQIRSQVMTLRVIYER 540
QY 541 MNOSLSLTVNPAVAEIODEVDELLOKEONYSDVLANMISEPRISYGDALMPSLTET 600
Db 541 MNOSLSLTVNPAVAEIODEVDELLOKEONYSDVLANMISEPRISYGDALMPSLTET 600
QY 601 KTVVELLPVNGEESLDLQPMHSGADSVAPANTENEVEPYDARPAADRGLTTPRGSLTN 660
Db 601 KTVVELLPVNGEESLDLQPMHSGADSVAPANTENEVEPYDARPAADRGLTTPRGSLTN 660
QY 661 IKTEEISEVKMDAEFRHDSGEYVNHOKLVFPADVGSNKCAITGLMVGVIATVITVL 720
Db 661 IKTEEISEVKMDAEFRHDSGEYVNHOKLVFPADVGSNKCAITGLMVGVIATVITVL 720
QY 721 VMLKKQYTSIHGGVGVDAVTPPEERHLSKMOONGENPTYKFEEDOMON 770
Db 721 VMLKKQYTSIHGGVGVDAVTPPEERHLSKMOONGENPTYKFEEDOMON 770

RESULT 9
AAU06622
ID AAU06622 standard; protein; 770 AA.

AC AAU06622;
DT 24-OCT-2001 (first entry)
XX Human partial Amyloid precursor protein, APP770.
DE Human; Aspartyl protease; Asp2; beta-secretase; neurotrophic;
XX neuroprotective; amyloid protein precursor; APP; Alzheimer's disease;
KW amyloid-beta; Abeta; APP770.
XX Homo sapiens.
OS
FT key Location/Qualifiers
MI Misc-difference 358 /note= "Encoded by GCC"
XX MO200149098-A2.
XX 12-JUL-2001.
XX 09-MAY-2001; 2001MO-IB00798.
XX 09-MAY-2001; 2001MO-IB00798.
XX 09-MAY-2001; 2001MO-IB00798.

PA (BIEN/) BIENKOWSKI M J.
PA (GURNEY/) GURNEY M E.
PA (HEIN/) HEINRIKSON R L.
PA (PARO/) PARODI L A.
PA (YANR/) YAN R.
XX BIENKOWSKI MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R.
XX MPI: 2001-502549/55.
XX N-PSDB: AAS11549.
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta

PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity -
XX Disclosure: page 171-173, 185pp; English.
XX The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp2) protein, which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp
CC proteins and vectors expressing them, and a polypeptide (isoform of
CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC APP or its fragment containing an APP cleavage site recognizable by a
CC mammalian beta-secretase, and further comprising two lysine residues at
CC the carboxyl terminus of the amino acid sequence of the mammalian APP or
CC APP fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. APP is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and
CC amyloid-beta (Abeta) peptide production. APP is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease.
CC APP comprising the APP-SV-beta-secretase peptide sequence (NIDA), which
CC is associated with increased levels of Abeta processing is useful in
CC assays relating to the Alzheimer's research. The expression vector is useful
CC for recombinantly expressing APP. Nucleic acids that hybridize to
CC APP oligonucleotides are useful as probes or primers. The probes are
CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence is human APP770.
XX Sequence 770 AA:
SQ

Query Match 100.0%; Score 4058; DB 22; Length 770;
Best Local Similarity 100.0%; Pred. No. 4.4e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNHNMYONGKMDSPSGTK 60
Db 1 MLEGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNHNMYONGKMDSPSGTK 60
QY 61 TCTIDTKEGILQYQOEYVPELOITNVVEANOPVITQWCKRGRKOCKTHRFVYPRCLVG 120
Db 61 TCTIDTKEGILQYQOEYVPELOITNVVEANOPVITQWCKRGRKOCKTHRFVYPRCLVG 120
QY 121 EYFSDALLVPDKCKFLHOERMVDCETHLHNTYAKETCSKSNLNDYGLLPCGIDKFR 180
Db 121 EYFSDALLVPDKCKFLHOERMVDCETHLHNTYAKETCSKSNLNDYGLLPCGIDKFR 180
QY 181 GVEFYCCPLAEESDNVDSADAEEDSDVMWCGADTDYADGSEBDKVVVEAEVEAEVEE 240
Db 181 GVEFYCCPLAEESDNVDSADAEEDSDVMWCGADTDYADGSEBDKVVVEAEVEAEVEE 240
QY 241 EADDDDDDDGDEVEEAEPEYEATEERTSTATTTTTTESVEEVVREVCQAETGRC 300
Db 241 EADDDDDDDGDEVEEAEPEYEATEERTSTATTTTTTESVEEVVREVCQAETGRC 300
QY 301 RAMISRMFYDVTGKCAPFFYGGCGGNRNPFDEEYCMVCGSAMQSILKTQOEPLARD 360
Db 301 RAMISRMFYDVTGKCAPFFYGGCGGNRNPFDEEYCMVCGSAMQSILKTQOEPLARD 360
QY 361 PVKLPTTAASTPDVADKYLETPEGDENEHAFQAKERLEAKHRRMSQVWREWEAEARQA 420
Db 361 PVKLPTTAASTPDVADKYLETPEGDENEHAFQAKERLEAKHRRMSQVWREWEAEARQA 420
QY 421 KNLPRADKRAVIOHFOEKVESLEOEANERQOLVETMARVEAMLNDRRLALENTYTL 480
Db 421 KNLPRADKRAVIOHFOEKVESLEOEANERQOLVETMARVEAMLNDRRLALENTYTL 480
QY 481 QAVPRPRHVFNMLKKYVAEOKDRQHTLKHFEHVAVMDPKAAQIRSQVMTLRVIYER 540
Db 481 QAVPRPRHVFNMLKKYVAEOKDRQHTLKHFEHVAVMDPKAAQIRSQVMTLRVIYER 540
QY 541 MNOSLSLTVNPAVAEIODEVDELLOKEONYSDVLANMISEPRISYGDALMPSLTET 600
Db 541 MNOSLSLTVNPAVAEIODEVDELLOKEONYSDVLANMISEPRISYGDALMPSLTET 600

ID	Accession	Protein Name	Length	Score	DB	Length	Score	DB
Db	541	MNOSLSLLYNPAVAEELIQDEVDDELQEQNSDDVLNMISEPRISVGNDAIMP	600					
Qy	601	KTVYELLVNGEFSIDDIQPMHSGADSVPAANTENEVEPVDARPAADGLTTRPGSGLTN	660					
Db	601	KTVYELLVNGEFSIDDIQPMHSGADSVPAANTENEVEPVDARPAADGLTTRPGSGLTN	660					
Qy	661	IKTEIISVKKDAERHRHSGYEVHHOKLVFPAEDVGSNKGALIGMVGVIATVITL	720					
Db	661	IKTEIISVKKDAERHRHSGYEVHHOKLVFPAEDVGSNKGALIGMVGVIATVITL	720					
Qy	721	VMLKKQTSIHGVEYDAAVTPPERHLSKMQQNGYENPTYKFEQMQN	770					
Db	721	VMLKKQTSIHGVEYDAAVTPPERHLSKMQQNGYENPTYKFEQMQN	770					
RESULT	10							
ID	AAE02600	AAE02600 standard; Protein, 770 AA.						
Accession	AAE02600							
Length	10-AUG-2001	(first entry)						
Protein Name	Human amyloid precursor protein 770 (App 770) protein.							
Human amyloid precursor protein 770 (App 770) protein.								
Human; alpha-secretase; amyloid precursor protein; App; therapy; Alzheimer's disease; antialzheimer's.								
Homo sapiens.								
Key	Location/Qualifiers							
Misc-difference 358	/note= "Encoded by GGC"							
WO200123533-A2.								
05-APR-2001.								
22-SEP-2000; 2000MO-US26080.								
23-SEP-1999; 99US-0155493.								
23-SEP-1999; 99MO-US20881.								
13-OCT-1999; 99US-0416901.								
06-DEC-1999; 99US-0169232.								
(PHAA) PHARMACIA & UPJOHN CO.								
Gurney M, Bienkowski MJ;								
WPI; 2001-290516//30.								
N-PSDB; AAD06770.								
Enzymes that cleave the alpha-secretase site of the amyloid precursor protein, useful for the treatment of Alzheimer's disease -								
Example 8; Page 170-172; 189pp; English.								
The present invention relates to enzymes for cleaving the alpha-secretase site of the amyloid precursor protein (APP) and methods of identifying those enzymes. The methods may be used to identify enzymes that may be used to cleave the alpha-secretase cleavage site of the APP protein. The enzymes may be used to treat or modulate the progress of Alzheimer's disease. The present sequence is human App 770 protein.								
Sequence	770 AA:							
Query Match	100.0%; Score 4058; DB 22; Length 770;							
Best Local Similarity	100.0%; Pred. No. 4.4e-289;							
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0.								
1	MLGGLALLLLAATVATRALEVPDGNGLIAEPDIAFCGRLLNHHMNVQNGKMDSDPSGTR	60						
1	MLGGLALLLLAATVATRALEVPDGNGLIAEPDIAFCGRLLNHHMNVQNGKMDSDPSGTR	60						

QY	61	TCIDTKESIIIDYCGEYVPELOITNVVNAPOVYTIOMCKRGRKQCKTHPHFVTPRCLVG	120		
Db	61	TCIDTKESIIIDYCGEYVPELOITNVVNAPOVYTIOMCKRGRKQCKTHPHFVTPRCLVG	120		
QY	121	EFVSDALLVPKCKFELHQRMDVCEYHLHMTYVAKETCSSEKSTNLDHYGMLDPCGIDKFR	180		
Db	121	EFVSDALLVPKCKFELHQRMDVCEYHLHMTYVAKETCSSEKSTNLDHYGMLDPCGIDKFR	180		
QY	181	GVEFVCGPLAEESDNDVSADAEEDSDVMWGMGADTDYADGSEDKVVEYAAEEEAVALVEEF	240		
Db	181	GVEFVCGPLAEESDNDVSADAEEDSDVMWGMGADTDYADGSEDKVVEYAAEEEAVALVEEF	240		
QY	241	EADDEDDEDDDEVEEAEAEPEYEATERTTSIATTTTTTSVEVVEVVEVSEQAEQPC	300		
Db	241	EADDEDDEDDDEVEEAEAEPEYEATERTTSIATTTTTTSVEVVEVVEVSEQAEQPC	300		
QY	301	RAMISRWVFDVTEGKCAFFYGGCGGNRNNDTEEYCAVAGSAMSOGLKTTQDEPLARD	360		
Db	301	RAMISRWVFDVTEGKCAFFYGGCGGNRNNDTEEYCAVAGSAMSOGLKTTQDEPLARD	360		
QY	361	PVKLPTTAASPPDAVDKLTLETPGDENEHAKAKERLEAHNREMSQVMKMEBAERQA	420		
Db	361	PVKLPTTAASPPDAVDKLTLETPGDENEHAKAKERLEAHNREMSQVMKMEBAERQA	420		
QY	421	KNLPRADKKAVYIQHQRKEVESLEQEAANEERQOLVETHNARVYEAMLNDRRLALENYITAL	480		
Db	421	KNLPRADKKAVYIQHQRKEVESLEQEAANEERQOLVETHNARVYEAMLNDRRLALENYITAL	480		
QY	481	QAVPRPRHVFENMLKKYVRAEOKDRQHTLKHFEHVRMYDPKKAQIRSOVMTHLYIER	540		
Db	481	QAVPRPRHVFENMLKKYVRAEOKDRQHTLKHFEHVRMYDPKKAQIRSOVMTHLYIER	540		
QY	541	NMOSILLYNPAVAEETODEVDELQKQBNYSDOVLNMTISEPTISYGNDAIAMSLEET	600		
Db	541	NMOSILLYNPAVAEETODEVDELQKQBNYSDOVLNMTISEPTISYGNDAIAMSLEET	600		
QY	601	KTTVELLPVNGEFSJDDIQQPMHSFGADSVAPANTENEVEPEVDARPAADRGLTTRPGSLTN	660		
Db	601	KTTVELLPVNGEFSJDDIQQPMHSFGADSVAPANTENEVEPEVDARPAADRGLTTRPGSLTN	660		
QY	661	IKTEEISEYKMDAEFRHDSGYEVHHQKLVFRAEDVGSNKGAIIIGLWGGVYIATYIVITL	720		
Db	661	IKTEEISEYKMDAEFRHDSGYEVHHQKLVFRAEDVGSNKGAIIIGLWGGVYIATYIVITL	720		
QY	721	VWLKKQYTSIHNGVGVENDAAVTPREHILSKMOQGYENPTYKFFEQMON	770		
Db	721	VWLKKQYTSIHNGVGVENDAAVTPREHILSKMOQGYENPTYKFFEQMON	770		
RESULT 11					
AAEL10650					
ID	AAEL10650 standard: Protein; 772 AA.				
XX	AAEL10650;				
XX	10-DEC-2001 (first entry)				
DE	Human amyloid protein precursor 770-KK (Aβ770-KK) isoform.				
KW	Human; aspartyl protease 1; Asp1; amyloid precursor protein; Aβ770-KK;				
KM	Alzheimer's disease; AD; dementia; neurofibrillary tangle; gliosis;				
XX	amyloid plaque; neuronal loss; proteolytic; neurotrophic; neuroprotective.				
OS	Homo sapiens.				
XX	Synthetic.				
PN	GB2357767-A.				
XX	04-JUL-2001.				
XX	22-SEP-2000; 2000GB-0023315.				
XX					

PR 23-SEP-1999; 9905-0155493.
 PR 23-SEP-1999; 9905-0404133.
 PR 23-SEP-1999; 9905-0520881.
 PR 13-OCT-1999; 9905-0416901.
 PR 06-DEC-1999; 9905-0169232.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 PI Bienkowski MJ, Gurney M;
 XX
 XX MPI; 2001-444208/48.
 DR N-PSDB; AAD17899.
 XX
 PT Polypeptide comprising fragments of human aspartyl protease with
 PT amyloid precursor protein processing activity and alpha-secretase
 PT activity, for identifying modulators useful in treating Alzheimer's
 PT disease -
 XX
 PS Disclosure: Page 148-151; 187pp; English.

The patent discloses human aspartyl protease 1 (hu-Asp1) or modified
 Asp1 proteins which lack transmembrane domain or amino terminal
 domain or cytoplasmic domain and retains alpha-secretase activity
 and amyloid protein precursor (APP) processing activity. The proteins
 of the invention are useful for assaying hu-Asp1 alpha-secretase
 activity, which in turn is useful for identifying modulators of
 hu-Asp1 alpha-secretase activity, where modulators that increase
 hu-Asp1 alpha-secretase activity are useful for treating Alzheimer's
 disease (AD) which causes progressive dementia with consequent
 formation of amyloid plaques, neurofibrillary tangles, gliosis and
 neuronal loss. Hu-Asp1 protease substrate is useful for assaying
 hu-Asp1 proteolytic activity, by contacting hu-Asp1 protein with
 the substrate under acidic conditions and determining the level of
 hu-Asp1 proteolytic activity. The present sequence is human amyloid
 protein precursor 770-KK (APP770-KK) isoform. APP770-KK isoform is
 obtained by the addition of two lys residues (KK motif) at the
 C-terminal of APP770 protein.

Sequence 772 AA:

Query Match 100.0%; Score 4058; DB 22; Length 772;
 Best Local Similarity 100.0%; Pred. No. 4.4e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MLEGLALLLLAATATATALEVPTDGNAGLLAEPOIAMFCGRLLNMHMYONCKMDSPEGK 60
 1 MLEGLALLLLAATATATALEVPTDGNAGLLAEPOIAMFCGRLLNMHMYONCKMDSPEGK 60
 DB 61 TCIDTKEGILQYCOEYVPELQITNVVEANQVPTIQNMCKRGKCKTNPFFVIRCLVG 120
 61 TCIDTKEGILQYCOEYVPELQITNVVEANQVPTIQNMCKRGKCKTNPFFVIRCLVG 120
 DB 121 EYVSDALVYDCKKFLHQRMDVCETHLHWYAKETCSKSTNLHDYGLMLPGIDKFR 180
 121 EYVSDALVYDCKKFLHQRMDVCETHLHWYAKETCSKSTNLHDYGLMLPGIDKFR 180
 DB 121 EYVSDALVYDCKKFLHQRMDVCETHLHWYAKETCSKSTNLHDYGLMLPGIDKFR 180
 121 EYVSDALVYDCKKFLHQRMDVCETHLHWYAKETCSKSTNLHDYGLMLPGIDKFR 180
 DB 181 GVEFVCCPLAEESDNDVSADAEEDSDVMWGADTYADSEDKVVAEEEAEEVEE 240
 181 GVEFVCCPLAEESDNDVSADAEEDSDVMWGADTYADSEDKVVAEEEAEEVEE 240
 DB 181 GVEFVCCPLAEESDNDVSADAEEDSDVMWGADTYADSEDKVVAEEEAEEVEE 240
 181 GVEFVCCPLAEESDNDVSADAEEDSDVMWGADTYADSEDKVVAEEEAEEVEE 240
 DB 241 EADDEDEDGDEVEEAEPYEBATERTTSIATTTTTTESVEEVVREYCSDEAETGPC 300
 241 EADDEDEDGDEVEEAEPYEBATERTTSIATTTTTTESVEEVVREYCSDEAETGPC 300
 DB 241 EADDEDEDGDEVEEAEPYEBATERTTSIATTTTTTESVEEVVREYCSDEAETGPC 300
 241 EADDEDEDGDEVEEAEPYEBATERTTSIATTTTTTESVEEVVREYCSDEAETGPC 300
 DB 301 RAMISRYEFTVTEGKCAPFYGGCGGNRNFDTEYCMACGSMQSLSLKTQOEPLARD 360
 301 RAMISRYEFTVTEGKCAPFYGGCGGNRNFDTEYCMACGSMQSLSLKTQOEPLARD 360
 DB 301 RAMISRYEFTVTEGKCAPFYGGCGGNRNFDTEYCMACGSMQSLSLKTQOEPLARD 360
 301 RAMISRYEFTVTEGKCAPFYGGCGGNRNFDTEYCMACGSMQSLSLKTQOEPLARD 360
 DB 361 PVKLPTTAATPAVDVLYLT PGDENHAFOKAKERLEKHKHRRMSQVAREEAEAROA 420
 361 PVKLPTTAATPAVDVLYLT PGDENHAFOKAKERLEKHKHRRMSQVAREEAEAROA 420
 DB 361 PVKLPTTAATPAVDVLYLT PGDENHAFOKAKERLEKHKHRRMSQVAREEAEAROA 420
 361 PVKLPTTAATPAVDVLYLT PGDENHAFOKAKERLEKHKHRRMSQVAREEAEAROA 420
 DB 421 KNLPKADKKAVIOHFQEKVESLEQEAANERQOLVETHMAREVAMLNDRRRLALENYITAL 480
 421 KNLPKADKKAVIOHFQEKVESLEQEAANERQOLVETHMAREVAMLNDRRRLALENYITAL 480

DB 421 KNLPKADKKAVIOHFQEKVESLEQEAANERQOLVETHMAREVAMLNDRRRLALENYITAL 480
 421 KNLPKADKKAVIOHFQEKVESLEQEAANERQOLVETHMAREVAMLNDRRRLALENYITAL 480
 DB 481 QAVPPRRHVFNNLKKYVRAEOKDRHTLKHFEHVAVRVPDKKAAQRSQVMTLRYIER 540
 481 QAVPPRRHVFNNLKKYVRAEOKDRHTLKHFEHVAVRVPDKKAAQRSQVMTLRYIER 540
 DB 481 QAVPPRRHVFNNLKKYVRAEOKDRHTLKHFEHVAVRVPDKKAAQRSQVMTLRYIER 540
 481 QAVPPRRHVFNNLKKYVRAEOKDRHTLKHFEHVAVRVPDKKAAQRSQVMTLRYIER 540
 DB 541 MNSLSLTVNPAVAEIOEVEDELQKEONYSDVYANNISPRISYGDALMPSTET 600
 541 MNSLSLTVNPAVAEIOEVEDELQKEONYSDVYANNISPRISYGDALMPSTET 600
 DB 541 MNSLSLTVNPAVAEIOEVEDELQKEONYSDVYANNISPRISYGDALMPSTET 600
 541 MNSLSLTVNPAVAEIOEVEDELQKEONYSDVYANNISPRISYGDALMPSTET 600
 DB 601 KTTVELLPVNGEESLDDLOPMHSFGADSVAPANTENEVEPYDAPRADRGITTRPGSLTN 660
 601 KTTVELLPVNGEESLDDLOPMHSFGADSVAPANTENEVEPYDAPRADRGITTRPGSLTN 660
 DB 601 KTTVELLPVNGEESLDDLOPMHSFGADSVAPANTENEVEPYDAPRADRGITTRPGSLTN 660
 601 KTTVELLPVNGEESLDDLOPMHSFGADSVAPANTENEVEPYDAPRADRGITTRPGSLTN 660
 DB 661 IKTEEISEVYMDAEFRHDSYEVYHOKLVFFADVGSNKCAIIGLVAGVIAIVITL 720
 661 IKTEEISEVYMDAEFRHDSYEVYHOKLVFFADVGSNKCAIIGLVAGVIAIVITL 720
 DB 661 IKTEEISEVYMDAEFRHDSYEVYHOKLVFFADVGSNKCAIIGLVAGVIAIVITL 720
 661 IKTEEISEVYMDAEFRHDSYEVYHOKLVFFADVGSNKCAIIGLVAGVIAIVITL 720
 DB 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMOONGENPTYKFFEDOMON 770
 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMOONGENPTYKFFEDOMON 770
 DB 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMOONGENPTYKFFEDOMON 770
 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMOONGENPTYKFFEDOMON 770

RESULT 12
 AAE06895
 ID AAE06895 standard; Protein; 772 AA.
 AC AAE06895;
 XX
 DT 23-OCT-2001 (first entry)
 XX
 DE Human amyloid precursor protein 770-KK (APP770-KK) isoform.
 XX
 KW Human; aspartyl protease; Asp; beta-amyloid precursor protein 770-KK;
 KW beta-secretase; Alzheimer's disease; dementia; amyloid plaque; gliosis;
 KW neurofibrillary tangle; neuronal loss; amyloid-beta peptide; neurotrophic;
 KW neuroprotective; antisense therapy; gene therapy; APP770-KK; mutant;
 KW muteln.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200150829-A2.
 XX
 PD 19-JUL-2001.
 XX
 PF 09-MAY-2001; 2001WO-1B00799.
 XX
 PR 09-MAY-2001; 2001WO-1B00799.
 XX
 PA (BIEN/) BIENKOWSKI M J.
 PA (GURN/) GURNEY M E.
 PA (HEIN/) HEINRIKSON R L.
 PA (PARO/) PARODI L A.
 PA (YANR/) YAN R.
 XX
 PI Bienkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;
 XX
 DR MPI; 2001-483072/52.
 DR N-PSDB; AAD13280.
 XX
 PT Novel purified polypeptide comprising fragment of mammalian aspartyl
 PT protease 2, lacking Asp2 transmembrane domain and retaining beta
 PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
 PT activity -
 XX
 PS Disclosure: Page 177-180; 185pp; English.
 XX
 CC The invention relates to human aspartyl proteases (Hu-Asp), beta-amyloid
 CC precursor protein (APP) isoforms and their corresponding DNA molecules.
 CC Human aspartyl proteases can act as beta-secretase proteases useful for
 CC treating Alzheimer's disease. App isoforms are useful for identifying

modulators of amyloid-beta peptide production, for use in designing therapeutics for the treatment and prevention of Alzheimer's disease, dementia, formation of amyloid plaques, neurofibrillary tangles, gliosis and neuronal loss. App isoforms are also used in methods for identifying inhibitors and modulators of human Asp2 activity. The invention relates to a method for identifying agents that modulate the activity of human aspartyl protease Asp2. Amyloid-beta peptides obtained from App are used as a means to screen in cellular assays for the inhibitors of beta- and gamma- secretase. Hu-Asp DNA fragments are useful as probes or primers in polymerase chain reactions (PCR). The probes are useful for detecting Hu-Asp nucleic acids in in vitro assays and in Northern and Southern blots. The present sequence is modified human amyloid precursor protein 770-Kk (App770-KK) isoform. App770-KK isoform is obtained by addition of two Lys residues (KK motif) at the C-terminal end of App770 isoform.

Query Match 100.0%; Score 4058; DB 22; Length 772;
Best Local Similarity 100.0%; Pred. No. 4.4e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRLGALLLAATATALEVPTDGNAGLLAEPOIAFCGRINMNMVONGKMDSPSGTK 60
1 MRLGALLLAATATALEVPTDGNAGLLAEPOIAFCGRINMNMVONGKMDSPSGTK 60
1 MRLGALLLAATATALEVPTDGNAGLLAEPOIAFCGRINMNMVONGKMDSPSGTK 60
61 TCIDTREGILQYCOEYVPELQITNVVEANOPVTIQNMCKRGKCKOCTHPHFVIRCLVG 120
61 TCIDTREGILQYCOEYVPELQITNVVEANOPVTIQNMCKRGKCKOCTHPHFVIRCLVG 120
121 EFVSDALLVPDKCKELHOEMDVCETHLHWHTAKETCSKSNLDYGLMPCGIDKPR 180
121 EFVSDALLVPDKCKELHOEMDVCETHLHWHTAKETCSKSNLDYGLMPCGIDKPR 180
121 EFVSDALLVPDKCKELHOEMDVCETHLHWHTAKETCSKSNLDYGLMPCGIDKPR 180
181 GVEVCCPLAEESDNDVSDAEEDSDVVMGAGADTDYADGSEDKVVEVAEEVEAEVEE 240
181 GVEVCCPLAEESDNDVSDAEEDSDVVMGAGADTDYADGSEDKVVEVAEEVEAEVEE 240
181 GVEVCCPLAEESDNDVSDAEEDSDVVMGAGADTDYADGSEDKVVEVAEEVEAEVEE 240
241 EADDDDEDDGDEVEEAEPEYEATERTSIATTTTTTSEVEVREVCSQAETGPC 300
241 EADDDDEDDGDEVEEAEPEYEATERTSIATTTTTTSEVEVREVCSQAETGPC 300
241 EADDDDEDDGDEVEEAEPEYEATERTSIATTTTTTSEVEVREVCSQAETGPC 300
301 RAMISRWYPTVTEGKCAPFYGGCGGRNMFDTBEVCMACGSMOSLTKTQEPRLARD 360
301 RAMISRWYPTVTEGKCAPFYGGCGGRNMFDTBEVCMACGSMOSLTKTQEPRLARD 360
301 RAMISRWYPTVTEGKCAPFYGGCGGRNMFDTBEVCMACGSMOSLTKTQEPRLARD 360
361 PVKLPPTTAASDPADVKKYLTPEGDENENAHFOKAKERLEAKHREMSQVAREVEAEERQA 420
361 PVKLPPTTAASDPADVKKYLTPEGDENENAHFOKAKERLEAKHREMSQVAREVEAEERQA 420
361 PVKLPPTTAASDPADVKKYLTPEGDENENAHFOKAKERLEAKHREMSQVAREVEAEERQA 420
421 KNLPRADKRAVIOHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENTTAL 480
421 KNLPRADKRAVIOHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENTTAL 480
421 KNLPRADKRAVIOHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRLALENTTAL 480
481 QAVPRPRRHVFNMLKKYVRAEOKRQOTLKHFEHVRAVDKKAQIRSOVTHLRYER 540
481 QAVPRPRRHVFNMLKKYVRAEOKRQOTLKHFEHVRAVDKKAQIRSOVTHLRYER 540
481 QAVPRPRRHVFNMLKKYVRAEOKRQOTLKHFEHVRAVDKKAQIRSOVTHLRYER 540
541 MNOSLSTLVNPAVAEIOEVDLQKEQNSDDVLANNISPRISYGDALMPSLTER 600
541 MNOSLSTLVNPAVAEIOEVDLQKEQNSDDVLANNISPRISYGDALMPSLTER 600
541 MNOSLSTLVNPAVAEIOEVDLQKEQNSDDVLANNISPRISYGDALMPSLTER 600
601 KTTVELLPVNGEFSLDLQFWHSFGADSVANTENVEYEPDARPADRGTLTRPGSGLTN 660
601 KTTVELLPVNGEFSLDLQFWHSFGADSVANTENVEYEPDARPADRGTLTRPGSGLTN 660
601 KTTVELLPVNGEFSLDLQFWHSFGADSVANTENVEYEPDARPADRGTLTRPGSGLTN 660
661 IKTEELISEVMDAEFRHDSGEVHNQKLVFAEDVGSNKCAITGLMGVAVIAIVITL 720
661 IKTEELISEVMDAEFRHDSGEVHNQKLVFAEDVGSNKCAITGLMGVAVIAIVITL 720
661 IKTEELISEVMDAEFRHDSGEVHNQKLVFAEDVGSNKCAITGLMGVAVIAIVITL 720
721 VMLKKKQYTSIHNGVVEVDAVTPREERHLSKMOONGYENPTYKFEEDMON 770
721 VMLKKKQYTSIHNGVVEVDAVTPREERHLSKMOONGYENPTYKFEEDMON 770
721 VMLKKKQYTSIHNGVVEVDAVTPREERHLSKMOONGYENPTYKFEEDMON 770

RESULT 13
AAU06624
ID AAU06624 standard; Protein; 772 AA.
AC AAU06624;
XX 24-OCT-2001 (first entry)
DT
XX Human Amyloid precursor protein mutant, App770-KK.
XX
XX Human; Aspartyl protease; Asp2b; beta-secretase; nototropic;
KW neuroprotective; amyloid protein precursor; App; Alzheimer's disease;
KW amyloid-beta; Abeta; App770-KK; mutant; mutlein.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 358
FT /note="Encoded by GCC"
FT Misc-difference 771..772
FT /note="2 Extra Lys residues added compared to
FT wild-type App770"
XX
XX WO200149098-A2.
XX
XX 12-JUL-2001.
XX
XX 09-MAY-2001; 2001WO-IB00798.
XX
XX 09-MAY-2001; 2001WO-IB00798.
PR
XX 09-MAY-2001; 2001WO-IB00798.
XX
XX (BIEN/) BIENKOWSKI M J.
PA (GURNEY/) GURNEY M E.
PA (HEINRIKSON/) HEINRIKSON R L.
PA (PARODI/) PARODI L A.
PA (YANR/) YAN R.
XX
XX Bienkowski MJ, Gurney ME, Heinrichson RL, Parodi LA, Yan R;
PI WPI; 2001-502549/55.
XX
XX Novel purified polypeptide comprising fragment of mammalian aspartyl
PT protease 2, lacking Asp2 transmembrane domain and retaining beta
PT secretase activity of Asp2 useful for identifying inhibitors of Asp2
PT activity
XX
XX Disclosure: Page 177-180; 185pp; English.
PS
XX The invention relates to a purified polypeptide comprising a fragment of
CC mammalian aspartyl protease (Asp)2 protein which lacks the Asp2
CC transmembrane domain and the Asp2 protein, and where the polypeptide and
CC the fragment retain the beta-secretase activity of the mammalian Asp2
CC protein. The invention also details polynucleotides for the Asp
CC proteins and vectors expressing them, and a polypeptide (isoform of
CC amyloid protein precursor (APP)) comprising the amino acid sequence of an
CC APP or its fragment containing an APP cleavage site recognizable by a
CC mammalian beta-secretase, and further comprising two lysine residues at
CC the carboxyl terminus of the amino acid sequence are methods of identifying
CC APP fragment. Also included in the invention are methods of identifying
CC modulators or inhibitors of Asp2. Modulators and inhibitors of Asp2 are
CC useful for treating Alzheimer's disease. App is useful in methods for
CC identifying inhibitors or modulators of human Asp2 activity and
CC amyloid-beta (Abeta) peptide production. App is also useful in designing
CC therapeutics for the treatment or prevention of Alzheimer's disease.
CC APP comprising the APP-SV-beta-secretase peptide sequence (NIDA), which
CC is associated with increased levels of Abeta processing is useful in
CC assays relating the Alzheimer's research. The expression vector is useful
CC for recombinantly expressing APP. Nucleic acids that hybridize to
CC Asp oligonucleotides are useful as probes or primers. The probes are
CC useful for detecting Hu-Asp nucleic acids in in vitro assays and in
CC Northern and Southern blots. The present sequence is the human
CC App770 mutant, App770-KK which has 2 extra Lys residues added at

CC the C-terminus compared to the wild-type APP770. The mutation alters the
 CC specificity of the APP gamma-secretase activity and increases the rate
 CC of processing of the amyloid Abeta peptide.

XX Sequence 772 AA:

Query Match 100.0%; Score 4058; DB 22; Length 772;
 Best Local Similarity 100.0%; Pred. No. 4.4e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHMYNQKWDSPSGTK 60
 DB 1 MLPGALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHMYNQKWDSPSGTK 60
 QY 61 TCIDTREGIIQYCOEYVPELOITNVVEANOPVTIONCKRGKROCKTHPFIYPRCLVG 120
 DB 61 TCIDTREGIIQYCOEYVPELOITNVVEANOPVTIONCKRGKROCKTHPFIYPRCLVG 120
 QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPGIDKFR 180
 QY 181 GVEVCCPLAEESDNVSADAEEDSDVMWGADTDYADGSEDKVVEAEVEAEVEE 240
 DB 181 GVEVCCPLAEESDNVSADAEEDSDVMWGADTDYADGSEDKVVEAEVEAEVEE 240
 QY 241 EADDEDEDEDEVEEAEPEEATEERTSITATTTTTSVEEYVREVSDEAETGPC 300
 DB 241 EADDEDEDEDEVEEAEPEEATEERTSITATTTTTSVEEYVREVSDEAETGPC 300
 QY 301 RAMISRYFDVTEGKCAPFYGGCGGNRNNDTEECYCAVGSAMSOGLTKTTOEPLARD 360
 DB 301 RAMISRYFDVTEGKCAPFYGGCGGNRNNDTEECYCAVGSAMSOGLTKTTOEPLARD 360
 QY 361 PVKLPPTAASPDVADVKLTLPDGENEHAHQAKERLEAHRHRMSQVMEAEAEQA 420
 DB 361 PVKLPPTAASPDVADVKLTLPDGENEHAHQAKERLEAHRHRMSQVMEAEAEQA 420
 QY 421 KNLKADKAVIQHFOEVESELEOEAANERQOLVETHARVEALNDRRLALENYITAL 480
 DB 421 KNLKADKAVIQHFOEVESELEOEAANERQOLVETHARVEALNDRRLALENYITAL 480
 QY 481 QAVPRPRHVEFMKLYVRAEQKDRHQLKHEHVRWVDPKKAQIRSOVTHLRYIER 540
 DB 481 QAVPRPRHVEFMKLYVRAEQKDRHQLKHEHVRWVDPKKAQIRSOVTHLRYIER 540
 QY 541 MNGSLILYNPVAVEIQDEVDLQEKQNTSDVLANMISEPRISYNDALMPSLET 600
 DB 541 MNGSLILYNPVAVEIQDEVDLQEKQNTSDVLANMISEPRISYNDALMPSLET 600
 QY 601 KTYVELLPVNGEESLDLQPHSGADSVAPANTENEVEPYAPARAARGLTRFGSGLTN 660
 DB 601 KTYVELLPVNGEESLDLQPHSGADSVAPANTENEVEPYAPARAARGLTRFGSGLTN 660
 QY 661 IKTEISEVKMDAFRRHDSGYEVHOKLVPEADVGSKGAILGLMVGVIATVIYTL 720
 DB 661 IKTEISEVKMDAFRRHDSGYEVHOKLVPEADVGSKGAILGLMVGVIATVIYTL 720
 QY 721 VMLKKKQYTSIHGCVVEADAATPEERHLSKMOONGYENPYKFEEDOMN 770
 DB 721 VMLKKKQYTSIHGCVVEADAATPEERHLSKMOONGYENPYKFEEDOMN 770

RESULT 14

AAU07223 standard; Protein: 772 AA.

AAU07223;

24-OCT-2001 (first entry)

Human beta-amyloid protein precursor, isoform APP770-KK.

KM Human: aspartyl protease 1; Asp-1; neurotrophic; neuroprotective;
 KM aspartyl protease 2; Asp2; amyloid protein precursor; APP;
 KM beta-secretase; Alzheimer's disease; APP770-KK.

OS Homo sapiens.

XX Key Location/Qualifiers
 XX MISC-difference 358
 XX /note="Encoded by ggc"

MO200149097-A2.

12-JUL-2001.

09-MAY-2001; 2001MO-IB00797.

09-MAY-2001; 2001MO-IB00797.

(BIEN/) BIENKOWSKI M J.

(GURN/) GURNEY M E.

(HEIN/) HEINRIKSON R L.

(PARO/) PARODI L A.

(YANR/) YAN R.

Blenkowski MJ, Gurney ME, Heinrikson RL, Parodi LA, Yan R;

WPI: 2001-502548/55.

N-P-SDB; NAA11736.

Novel purified polypeptide comprising fragment of mammalian aspartyl

protease 2, lacking Asp2 transmembrane domain and retaining beta

secretase activity of Asp2 useful for identifying inhibitors of Asp2

activity

Disclosure: Page 177-180; 185pp; English.

The invention relates to a novel purified polypeptide comprising a

fragment of mammalian aspartyl protease 2 (Asp2) protein which lacks the

Asp2 transmembrane domain and the Asp2 protein, and where the polypeptide

and the fragment retain the beta-secretase activity of the mammalian Asp2

protein. Also included is an isoform of a APP or its fragment containing

comprising the amino acid sequence of a APP or its fragment containing

an APP cleavage site recognizable by a mammalian beta-secretase, and

further comprising two lysine residues at the carboxyl terminus of the

amino acid sequence of the mammalian APP or APP fragment. The

polypeptides are used for assaying for modulators of beta-secretase

activity; identifying agents that inhibit the APP processing activity

of human Asp2 aspartyl protease (Hu-Asp2); identifying agents that

modulate the activity of Asp2; and for reducing cellular production of

amyloid beta (Abeta) from APP. Agents identified by the above methods

are useful for treating Alzheimer's disease; and for identifying

modulators of amyloid beta (Abeta) peptide production, for use in

designing therapeutics for the treatment or prevention of Alzheimer's

disease. Probes and primers derived from Asp nucleic acid sequences

are useful for detecting Hu-Asp nucleic acids in in vitro assays and in

Northern and Southern blots. The present sequence represents the amino

acid sequence of human amyloid protein precursor, isoform APP770-KK,

used in the method of the invention.

Sequence 772 AA:

Query Match 100.0%; Score 4058; DB 22; Length 772;
 Best Local Similarity 100.0%; Pred. No. 4.4e-289;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPGALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHMYNQKWDSPSGTK 60
 DB 1 MLPGALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRNLNMHMYNQKWDSPSGTK 60
 QY 61 TCIDTREGIIQYCOEYVPELOITNVVEANOPVTIONCKRGKROCKTHPFIYPRCLVG 120
 DB 61 TCIDTREGIIQYCOEYVPELOITNVVEANOPVTIONCKRGKROCKTHPFIYPRCLVG 120


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QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMTYAKETCSKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMTYAKETCSKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAEESDNVSADAEEDSDVMWGADTDYADSEDEKVVVAEEVEAEVEEE 240
DB 181 GVEFVCCPLAEESDNVSADAEEDSDVMWGADTDYADSEDEKVVVAEEVEAEVEEE 240
QY 241 EADDEDDEDEGEVEEAEEPEYEATERTSIATTTTTTTSVEVEVREVCSEDAETGPC 300
DB 241 EADDEDDEDEGEVEEAEEPEYEATERTSIATTTTTTTSVEVEVREVCSEDAETGPC 300
QY 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNDTEYCMAYGSAVSQSLKTTQDEPLARD 360
DB 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNDTEYCMAYGSAVSQSLKTTQDEPLARD 360
QY 361 PVKLPPTAASTPDADVDTLETPGDENENAHFOKAKERLEAKHRRMSQVNRMEAEARQA 420
DB 361 PVKLPPTAASTPDADVDTLETPGDENENAHFOKAKERLEAKHRRMSQVNRMEAEARQA 420
QY 421 KNLPRADKKAIVIOHFOEKVESLEQEAANERQQLVETMARVEAMLNDRRLALENYITAL 480
DB 421 KNLPRADKKAIVIOHFOEKVESLEQEAANERQQLVETMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPRPRRHVFNMLKKTVYRAEQKDRQHTLKHFEHVRWVDPKKAQIISQVWTHLRVIYER 540
DB 481 QAVPRPRRHVFNMLKKTVYRAEQKDRQHTLKHFEHVRWVDPKKAQIISQVWTHLRVIYER 540
QY 541 MNOSLSLLYNPAVAEEIODEVDELLOKEQNSDVLANMISEPRISYGDALMPSLLET 600
DB 541 MNOSLSLLYNPAVAEEIODEVDELLOKEQNSDVLANMISEPRISYGDALMPSLLET 600
QY 601 KTVTELLPVNGEESLDDLOPHWSFGADSVPAANTEVEVEPYDARPAADRGGLTRRGSGLTN 660
DB 601 KTVTELLPVNGEESLDDLOPHWSFGADSVPAANTEVEVEPYDARPAADRGGLTRRGSGLTN 660
QY 661 IKTEEISEVKMDADEFRRDSGVEVHHOKLYPFAEDVGSNKGAIIGLAMGGVIAIVITTL 720
DB 661 IKTEEISEVKMDADEFRRDSGVEVHHOKLYPFAEDVGSNKGAIIGLAMGGVIAIVITTL 720
QY 721 VMLKKQYTSIHGIVVEYDAVTPPEERHLSKMQONGYENPTYKFFPEQMON 770
DB 721 VMLKKQYTSIHGIVVEYDAVTPPEERHLSKMQONGYENPTYKFFPEQMON 770

```

RESULT 15
AAE02602 standard; Protein; 772 AA.

AAE02602;

10-AUG-2001 (first entry)

Human amyloid precursor protein 770-KK (App 770-KK) protein.

Human: alpha-secretase; amyloid precursor protein; APP; therapy;
Alzheimer's disease; antialzheimer's.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 358 /note= "Encoded by GGC"

MO200123533-A2.

05-Apr-2001.

22-SEP-2000; 2000MO-US26080.

23-SEP-1999; 99US-0155493.

23-SEP-1999; 99MO-US20881.

13-OCT-1999; 99US-0416901.

```

PR 06-DEC-1999; 99US-0169232.
PA (PHAA) PHARMACIA & UPJOHN CO.
XX Gurney M, Bienkowski MJ;
PI WPI, 2001-290516/30.
XX N-PSDB; AAD06772.
DR
XX Enzymes that cleave the alpha-secretase site of the amyloid precursor
PT protein, useful for the treatment of Alzheimer's disease.
XX
XX Example 8; Page 176-179; 189pp; English.
XX
XX The present invention relates to enzymes for cleaving the alpha-
CC secretase site of the amyloid precursor protein (APP) and methods of
CC identifying these enzymes. The methods may be used to identify enzymes
CC that may be used to cleave the alpha-secretase cleavage site of the APP
CC protein. The enzymes may be used to treat or modulate the progress of
CC Alzheimer's disease. The present sequence is human APP 770-KK protein.
XX
XX Sequence 772 AA:
SQ
Query Match 100.0%; Score 4058; DB 22; Length 772;
Best Local Similarity 100.0%; Pred. No. 4, 4e-289;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLEGLALLLAAMTARALEVPTDGNAGLAEPOIAMFCGRILNMHMVONGKWDSPSGTK 60
DB 1 MLEGLALLLAAMTARALEVPTDGNAGLAEPOIAMFCGRILNMHMVONGKWDSPSGTK 60
QY 61 TCIDTKKGIIQYCOEYVPELIQTNVVEANQVITQNNCKRGKQCKTHPHFVIRCLYG 120
DB 61 TCIDTKKGIIQYCOEYVPELIQTNVVEANQVITQNNCKRGKQCKTHPHFVIRCLYG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMTYAKETCSKSTNLHDYGMLLPGCIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMTYAKETCSKSTNLHDYGMLLPGCIDKFR 180
QY 181 GVEFVCCPLAEESDNVSADAEEDSDVMWGADTDYADSEDEKVVVAEEVEAEVEEE 240
DB 181 GVEFVCCPLAEESDNVSADAEEDSDVMWGADTDYADSEDEKVVVAEEVEAEVEEE 240
QY 241 EADDEDDEDEGEVEEAEEPEYEATERTSIATTTTTTTSVEVEVREVCSEDAETGPC 300
DB 241 EADDEDDEDEGEVEEAEEPEYEATERTSIATTTTTTTSVEVEVREVCSEDAETGPC 300
QY 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNDTEYCMAYGSAVSQSLKTTQDEPLARD 360
DB 301 RAMISRWYFDVTEGKCAPFFYGGCGGNRNNDTEYCMAYGSAVSQSLKTTQDEPLARD 360
QY 361 PVKLPPTAASTPDADVDTLETPGDENENAHFOKAKERLEAKHRRMSQVNRMEAEARQA 420
DB 361 PVKLPPTAASTPDADVDTLETPGDENENAHFOKAKERLEAKHRRMSQVNRMEAEARQA 420
QY 421 KNLPRADKKAIVIOHFOEKVESLEQEAANERQQLVETMARVEAMLNDRRLALENYITAL 480
DB 421 KNLPRADKKAIVIOHFOEKVESLEQEAANERQQLVETMARVEAMLNDRRLALENYITAL 480
QY 481 QAVPRPRRHVFNMLKKTVYRAEQKDRQHTLKHFEHVRWVDPKKAQIISQVWTHLRVIYER 540
DB 481 QAVPRPRRHVFNMLKKTVYRAEQKDRQHTLKHFEHVRWVDPKKAQIISQVWTHLRVIYER 540
QY 541 MNOSLSLLYNPAVAEEIODEVDELLOKEQNSDVLANMISEPRISYGDALMPSLLET 600
DB 541 MNOSLSLLYNPAVAEEIODEVDELLOKEQNSDVLANMISEPRISYGDALMPSLLET 600
QY 601 KTVTELLPVNGEESLDDLOPHWSFGADSVPAANTEVEVEPYDARPAADRGGLTRRGSGLTN 660
DB 601 KTVTELLPVNGEESLDDLOPHWSFGADSVPAANTEVEVEPYDARPAADRGGLTRRGSGLTN 660
QY 661 IKTEEISEVKMDADEFRRDSGVEVHHOKLYPFAEDVGSNKGAIIGLAMGGVIAIVITTL 720
DB 661 IKTEEISEVKMDADEFRRDSGVEVHHOKLYPFAEDVGSNKGAIIGLAMGGVIAIVITTL 720

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Thu Oct 31 10:41:44 2002

us-09-785-215-2.rag

Page 14

Db 661 IKTEBISVKKDAEPRHDSGVENHÖKLVPFAELVSGSNKAIIGLMGVIVATVITL 720

0Y 721 VMLKKQYTSIHHGV EYDAVTPDEERHLSKMOONGYENPTYKFEEDOMN 770

Dd 721 VMLKKQYTSIHHGV EYDAVTPDEERHLSKMOONGYENPTYKFEEDOMN 770

Search completed: October 31, 2002, 10:11:59
Job time : 57.9852 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:56 ; Search time 20.8364 Seconds
(without alignments)
902.637 Million cell updates/sec

Title: US-09-785-215-2

Perfect score: 4058
Sequence: 1 MLPGLALLLAAMTARALEV.....KMOONGYENPTYKFEQMON 770

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues
Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Issued Patents, AA: *
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/prodata/1/1aa/5A_COMB.pep: *
4: /cgn2_6/prodata/1/1aa/5B_COMB.pep: *
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/prodata/1/1aa/Backfillsl.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4058	100.0	770	1	US-08-133-248-8
2	4058	100.0	770	1	US-08-231-940-1
3	4058	100.0	770	2	US-08-641-774-1
4	4058	100.0	770	2	US-08-104-165-3
5	4058	100.0	770	3	US-08-464-250-3
6	4058	100.0	770	4	US-08-464-250-3
7	3943.5	97.2	751	1	US-08-123-702-4
8	3943.5	97.2	751	2	US-08-104-165-2
9	3943.5	97.2	751	2	US-08-422-333-21
10	3943.5	97.2	751	2	US-08-422-333-21
11	3943.5	97.2	751	3	US-08-464-250-2
12	3943.5	97.2	751	4	US-08-464-250-2
13	3943.5	97.2	751	6	5187153-2
14	3943.5	97.2	751	6	5223482-2
15	3937.5	97.0	751	6	5220013-2
16	3590.5	88.5	695	1	US-08-123-702-2
17	3590.5	88.5	695	2	US-08-104-165-1
18	3590.5	88.5	695	3	US-08-464-250-1
19	3590.5	88.5	695	4	US-08-464-250-1
20	3590.5	88.5	695	4	US-09-458-481B-7
21	3590.5	88.5	695	4	US-09-458-481B-8
22	3590.5	88.5	695	6	5218100-2
23	3584.5	88.3	694	1	US-08-339-152A-18
24	3584.5	88.3	694	2	US-08-007-999B-5
25	3584.5	88.3	694	2	US-08-689-276A-5
26	3578.5	88.2	695	1	US-08-371-930-27
27	3578.5	88.2	695	5	PCT-US94-01712-27

28	3566.5	87.9	695	1	US-08-339-152A-30	Sequence 30, Appl
29	3493.5	86.1	695	4	US-09-458-481B-6	Sequence 6, Appl
30	3489.5	86.0	695	4	US-09-458-481B-4	Sequence 4, Appl
31	3471.5	85.5	676	1	US-08-371-930-24	Sequence 24, Appl
32	3471.5	85.5	676	5	PCT-US94-01712-24	Sequence 24, Appl
33	3468.5	85.5	695	4	US-09-458-481B-5	Sequence 5, Appl
34	3366.5	83.0	656	1	US-08-371-930-23	Sequence 23, Appl
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36	3356.5	82.7	1024	4	US-09-522-666-2	Sequence 2, Appl
37	2393.5	59.0	487	1	US-08-462-859A-9	Sequence 9, Appl
38	2393.5	59.0	487	1	US-08-123-659A-9	Sequence 9, Appl
39	2393.5	59.0	487	1	US-08-464-247A-9	Sequence 9, Appl
40	2393.5	59.0	487	1	US-08-464-248A-9	Sequence 9, Appl
41	2393.5	59.0	492	1	US-08-462-859A-7	Sequence 7, Appl
42	2393.5	59.0	492	1	US-08-123-659A-7	Sequence 7, Appl
43	2393.5	59.0	492	1	US-08-464-247A-7	Sequence 7, Appl
44	2393.5	59.0	492	1	US-08-464-248A-7	Sequence 7, Appl
45	1975.5	48.7	763	1	US-08-155-331-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1									
US-08-133-248-8									
Sequence 8, Application US/08133248									
Patent No. 5525714									
GENERAL INFORMATION:									
APPLICANT:									
TITLE OF INVENTION: MUTATED FORM OF THE BETA-AMYLOID PRECURSOR									
TITLE OF INVENTION: PROTEIN GENE									
NUMBER OF SEQUENCES: 8									
COMPUTER READABLE FORM:									
MEDIUM TYPE: Floppy disk									
COMPUTER: IBM PC compatible									
OPERATING SYSTEM: PC-DOS/MS-DOS									
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)									
CURRENT APPLICATION DATA:									
APPLICATION NUMBER: US/08/133,248									
INFORMATION FOR SEQ ID NO: 8:									
SEQUENCE CHARACTERISTICS:									
LENGTH: 770 amino acids									
TYPE: amino acid									
TOPOLOGY: linear									
MOLECULE TYPE: protein									
US-08-133-248-8									
Query Match									
Best Local Similarity 100.0%; Score 4058; DB 1; Length 770;									
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	1	MLPGLALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRILNMHMNVONGKWDSPSGTK	60						
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DB	61	TCIDTKSGITQYQOEYRELPQITNNVYANOPVITQNNCKRGKQCKNHPFVIRPLVGL	120						
QY	121	EFPSDALLVDPKCKFLQOEMNDVCETLHMHTYAKETCSKSTLHJYGMILPCGIDKFR	180						
DB	121	EFPSDALLVDPKCKFLQOEMNDVCETLHMHTYAKETCSKSTLHJYGMILPCGIDKFR	180						
QY	181	GVEFYCCPLAEESDNVDSADAEEDSDVMWGGADTDYADSEDKVVEAEVEEVAEVEE	240						
DB	181	GVEFYCCPLAEESDNVDSADAEEDSDVMWGGADTDYADSEDKVVEAEVEEVAEVEE	240						
QY	241	EADDEDDEGDEVEEAEPYERATRTSIAITTTTTSVEVYRVCSBDAEFGPC	300						
DB	241	EADDEDDEGDEVEEAEPYERATRTSIAITTTTTSVEVYRVCSBDAEFGPC	300						
QY	301	RAMISRYFPVTSKCKAPFYGGCGGRNPNDFEYGMAYGVSMSQSLKTQDEPLARD	360						
DB	301	RAMISRYFPVTSKCKAPFYGGCGGRNPNDFEYGMAYGVSMSQSLKTQDEPLARD	360						

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Db 301 RAMISRMVFDVTEGKCAPFFYGGCGNRNNFDETEYCMANVGSAMSOSLTKTTOEPLARD 360
Qy 361 PVKLPPTAASPDAVDKYLETPGDENENAHFQAKERLEKAKHRMSQVMREWEAEAROA 420
Db 361 PVKLPPTAASPDAVDKYLETPGDENENAHFQAKERLEKAKHRMSQVMREWEAEAROA 420
Qy 421 KNLPRADKKAIVIOHFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRRLALENYITL 480
Db 421 KNLPRADKKAIVIOHFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRRLALENYITL 480
Qy 481 QAVPRPRHVFNNMLKKYVRAEQKROHTLKHFEHVRVMDPKKAAQIRSOVMTLRYIYER 540
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Qy 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFPAEDVGSNKGAITGLMVGVIATVITL 720
Db 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFPAEDVGSNKGAITGLMVGVIATVITL 720
Qy 721 VMLKKROYTSIHGVEVDAVAVTPEERHLSKMOONGYENPTYKFEFQOMON 770
Db 721 VMLKKROYTSIHGVEVDAVAVTPEERHLSKMOONGYENPTYKFEFQOMON 770

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RESULT 2

US-08-231-940-1

; Sequence 1, Application US/08231940

; Patent No. 5550216

; GENERAL INFORMATION:

; APPLICANT: MIYAZAKI, Kaoru

; TITLE OF INVENTION: GELATINASE A INHIBITOR

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/231,940

; FILING DATE: 25-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 5-120457

; FILING DATE: 26-APR-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 6-62129

; FILING DATE: 08-MAR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: NEIMARK, Sheridan

; REGISTRATION NUMBER: 20,520

; REFERENCE/DOCKET NUMBER: MIYAZAKI-4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; TELEX: 248633

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 770 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-231-940-1

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Query Match 100.0%; Score 4058; DB 1; Length 770;

Best Local Similarity 100.0%; Pred. No. 5,8e-281;

Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MRLGALMLLLAATPARLEVPDTGNAGLLAEPOIAMCGRLNMNMVONKMPDSPECTK 60
Db 1 MRLGALMLLLAATPARLEVPDTGNAGLLAEPOIAMCGRLNMNMVONKMPDSPECTK 60
Qy 61 TCIDTEKGLIQOCEYVPELOITNVVEANQPVITONCKGKRQCKTHPFVIRPLGV 120
Db 61 TCIDTEKGLIQOCEYVPELOITNVVEANQPVITONCKGKRQCKTHPFVIRPLGV 120
Qy 121 EYVSDALVVDKCKFLHOERMDVCEYLHWHYVAKETCSKSTNLHDYGMLLPCGIDKFR 180
Db 121 EYVSDALVVDKCKFLHOERMDVCEYLHWHYVAKETCSKSTNLHDYGMLLPCGIDKFR 180
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Db 181 GVEFVCCPLAEESDNDSDADAEEDSDVMWGADTDADGSEDKVVEVAEEEAEEVEE 240
Qy 241 EADDDDEDEDEGDEVEEAEERPEATEERTSIAITTTTTESEVEEVREVCSQAETGPC 300
Db 241 EADDDDEDEDEGDEVEEAEERPEATEERTSIAITTTTTESEVEEVREVCSQAETGPC 300
Qy 301 RAMISRMVFDVTEGKCAPFFYGGCGGNRNNFDETEYCMANVGSAMSOSLTKTTOEPLARD 360
Db 301 RAMISRMVFDVTEGKCAPFFYGGCGGNRNNFDETEYCMANVGSAMSOSLTKTTOEPLARD 360
Qy 361 PVKLPPTAASPDAVDKYLETPGDENENAHFQAKERLEKAKHRMSQVMREWEAEAROA 420
Db 361 PVKLPPTAASPDAVDKYLETPGDENENAHFQAKERLEKAKHRMSQVMREWEAEAROA 420
Qy 421 KNLPRADKKAIVIOHFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRRLALENYITL 480
Db 421 KNLPRADKKAIVIOHFQEKVESLEQEAANERQOLVETHMARVEAMLNDRRRLALENYITL 480
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Db 481 QAVPRPRHVFNNMLKKYVRAEQKROHTLKHFEHVRVMDPKKAAQIRSOVMTLRYIYER 540
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Db 541 MNSLSLTVNPAVAEIODEVDELQKEONYSDDVLANMISEPRISYGDALMPSLTET 600
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Db 601 KTVVELLPVNGEFSLDLQPMHSGADSVAPANTENEVEPYDARPADRGLTTRPGSLTN 660
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Db 661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFPAEDVGSNKGAITGLMVGVIATVITL 720
Qy 721 VMLKKROYTSIHGVEVDAVAVTPEERHLSKMOONGYENPTYKFEFQOMON 770
Db 721 VMLKKROYTSIHGVEVDAVAVTPEERHLSKMOONGYENPTYKFEFQOMON 770

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RESULT 3

US-08-641-774-1

; Sequence 1, Application US/08641774

; Patent No. 5843695

; GENERAL INFORMATION:

; APPLICANT: MIYAZAKI, Kaoru

; TITLE OF INVENTION: BETA-AP DECOMPOSING AGENT

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK

; STREET: 419 Seventh Street, N.W., Suite 300

; CITY: Washington

```

STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/641,774
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,474
FILING DATE: 25-APR-1994
APPLICATION NUMBER: JP 5-122207
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-51133
FILING DATE: 08-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: NEIMARK, Sheridan
REGISTRATION NUMBER: 20,520
REFERENCE/DOCKET NUMBER: MIYAZAKI-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-641-774-1

Query Match      100.0%; Score 4058; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 5,8e-281;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 481 QAVPRPRHVFNMKKYVRAEQDKROHTLKHFEHVNRVDPKKAQIRSQVMTLRLVIYER 540
QY 541 MNOSLLYNVPAVAEIODEVDELQKEONYSDVLANNISPRISYGDALMPSITET 600
DB 541 MNOSLLYNVPAVAEIODEVDELQKEONYSDVLANNISPRISYGDALMPSITET 600
QY 601 KTTVELLPVNGEFLDLOPWHSGADSVANTENEPVDPARADRGILTRPGSLTN 660
DB 601 KTTVELLPVNGEFLDLOPWHSGADSVANTENEPVDPARADRGILTRPGSLTN 660
QY 661 IKTEEISEVKNDAEFRRDSGEVHOKLVFEARDVGSNKGAIIGLWGVVIAVITL 720
DB 661 IKTEEISEVKNDAEFRRDSGEVHOKLVFEARDVGSNKGAIIGLWGVVIAVITL 720
QY 721 VMLKKQYTSIHGGVVEVDAVTPPEERHLSKMOONGYENPTFFEQMQN 770
DB 721 VMLKKQYTSIHGGVVEVDAVTPPEERHLSKMOONGYENPTFFEQMQN 770

RESULT 4
US-08-104-165-3
Sequence 3, Application US/08104165
Patent No. 5877015
GENERAL INFORMATION:
APPLICANT: HARDY, John Anthony
APPLICANT: GOATE, Allison Mary
APPLICANT: MULLAN, Michael John
APPLICANT: CHARTER-HARLIN, Marie-Christine
APPLICANT: OWEN, Michael John
TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/104,165
FILING DATE: 21-JAN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16163-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-104-165-3

Query Match      100.0%; Score 4058; DB 2; Length 770;
Best Local Similarity 100.0%; Pred. No. 5,8e-281;
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MLPGALLLLAAMTARALEVPTDGNAGLLAPQIAMFCGLNMHMNVQNGKWDSPSTK 60
QY 61 TCIDTKREGIILOCOEYVPELOITNVVEANOPTYIIONMCKRGRCKOCTHPHFVIRCLVG 120
DB 61 TCIDTKREGIILOCOEYVPELOITNVVEANOPTYIIONMCKRGRCKOCTHPHFVIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCEETHLHMHTVAKETCSKSTNLHDYGMLLPGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCEETHLHMHTVAKETCSKSTNLHDYGMLLPGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEBDDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEBDDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDEDEDEDEGEVEEAEPYEEATEERTSIAITTTTTTSEVEEYVREVCSEDAETGPC 300
DB 241 EADDEDEDEDEGEVEEAEPYEEATEERTSIAITTTTTTSEVEEYVREVCSEDAETGPC 300
QY 301 RAMISRWYFDVTEGKCAPFFYGGGGRNNNDTEECYCAVCGSAMSOGLKTQEPILARD 360
DB 301 RAMISRWYFDVTEGKCAPFFYGGGGRNNNDTEECYCAVCGSAMSOGLKTQEPILARD 360
QY 361 PVKLPTTAASTPDAVDKYLETGPDENENAHFOKAKERLEAKHREMSQVWREWEAEARQA 420
DB 361 PVKLPTTAASTPDAVDKYLETGPDENENAHFOKAKERLEAKHREMSQVWREWEAEARQA 420
QY 421 KNLPRADKKAVIOHFOEKVESLEODANERQOVLVTHMARVEAMLNDRRRLALENYITAL 480
DB 421 KNLPRADKKAVIOHFOEKVESLEODANERQOVLVTHMARVEAMLNDRRRLALENYITAL 480
QY 481 QAVPRRHHVFNMLKKYVRAQKROHTLKHFEHVWVDPKKAQIRSOVTHIRVIER 540
DB 481 QAVPRRHHVFNMLKKYVRAQKROHTLKHFEHVWVDPKKAQIRSOVTHIRVIER 540
QY 541 MNOSLSLLYNVPAVAEIEODEVELLOKEONYSDVLANMISEPRISYGNALMPSLJET 600
DB 541 MNOSLSLLYNVPAVAEIEODEVELLOKEONYSDVLANMISEPRISYGNALMPSLJET 600
QY 601 KTYVELLPVNGEESLDLQPHNSFGADSVPRANTENEVEPVDPARAARGLTTRGSGITN 660
DB 601 KTYVELLPVNGEESLDLQPHNSFGADSVPRANTENEVEPVDPARAARGLTTRGSGITN 660
QY 661 IKTEISEVKMDAEFRHDSGEVHHOKLVFPAEDVGSNKGAIIIGLAVGVIAIVYITL 720
DB 661 IKTEISEVKMDAEFRHDSGEVHHOKLVFPAEDVGSNKGAIIIGLAVGVIAIVYITL 720
QY 721 VMLKKKOYTSIHGVEVDAVTPERHLSKMOONGYENPTYKFEQMON 770
DB 721 VMLKKKOYTSIHGVEVDAVTPERHLSKMOONGYENPTYKFEQMON 770

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RESULT 5

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US-08-464-250-3
Sequence 3, Application US/08464250
Patent No. 6107542
GENERAL INFORMATION:
APPLICANT: HARDY, John Anthony
APPLICANT: COATE, Alison Mary
APPLICANT: MULLAN, Michael John
APPLICANT: CHARTIER-HARLIN, Marie-Christine
APPLICANT: OWEN, Michael John
TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,250
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/104,165
FILING DATE: 21-JAN-1992
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16163-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-250-3
Query Match 100.0%; Score 4058; DB 3; Length 770;
Best Local Similarity 100.0%; Pred. No. 5 8e-281.
Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLPGALLLLAAMTARALEVPTDGNAGLLAPQIAMFCGLNMHMNVQNGKWDSPSTK 60
DB 1 MLPGALLLLAAMTARALEVPTDGNAGLLAPQIAMFCGLNMHMNVQNGKWDSPSTK 60
QY 61 TCIDTKREGIILOCOEYVPELOITNVVEANOPTYIIONMCKRGRCKOCTHPHFVIRCLVG 120
DB 61 TCIDTKREGIILOCOEYVPELOITNVVEANOPTYIIONMCKRGRCKOCTHPHFVIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCEETHLHMHTVAKETCSKSTNLHDYGMLLPGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCEETHLHMHTVAKETCSKSTNLHDYGMLLPGIDKFR 180
QY 181 GVEFVCCPLAEESDNVDSADAEBDDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
DB 181 GVEFVCCPLAEESDNVDSADAEBDDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEE 240
QY 241 EADDEDEDEDEGEVEEAEPYEEATEERTSIAITTTTTTSEVEEYVREVCSEDAETGPC 300
DB 241 EADDEDEDEDEGEVEEAEPYEEATEERTSIAITTTTTTSEVEEYVREVCSEDAETGPC 300
QY 301 RAMISRWYFDVTEGKCAPFFYGGGGRNNNDTEECYCAVCGSAMSOGLKTQEPILARD 360
DB 301 RAMISRWYFDVTEGKCAPFFYGGGGRNNNDTEECYCAVCGSAMSOGLKTQEPILARD 360
QY 361 PVKLPTTAASTPDAVDKYLETGPDENENAHFOKAKERLEAKHREMSQVWREWEAEARQA 420
DB 361 PVKLPTTAASTPDAVDKYLETGPDENENAHFOKAKERLEAKHREMSQVWREWEAEARQA 420
QY 421 KNLPRADKKAVIOHFOEKVESLEODANERQOVLVTHMARVEAMLNDRRRLALENYITAL 480
DB 421 KNLPRADKKAVIOHFOEKVESLEODANERQOVLVTHMARVEAMLNDRRRLALENYITAL 480
QY 481 QAVPRRHHVFNMLKKYVRAQKROHTLKHFEHVWVDPKKAQIRSOVTHIRVIER 540
DB 481 QAVPRRHHVFNMLKKYVRAQKROHTLKHFEHVWVDPKKAQIRSOVTHIRVIER 540
QY 541 MNOSLSLLYNVPAVAEIEODEVELLOKEONYSDVLANMISEPRISYGNALMPSLJET 600
DB 541 MNOSLSLLYNVPAVAEIEODEVELLOKEONYSDVLANMISEPRISYGNALMPSLJET 600

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QY 601 KTTVELLPVNGEESLDLOQWHSFGADSVAPANTENEVEPYDARPADRGLTTRPGSLTN 660
 DB 601 KTTVELLPVNGEESLDLOQWHSFGADSVAPANTENEVEPYDARPADRGLTTRPGSLTN 660
 QY 661 IKTEEISEVMDAEFRHDSGEYVHOKLVFPAEDVGSNKGAIIGLMGVVIATVITL 720
 DB 661 IKTEEISEVMDAEFRHDSGEYVHOKLVFPAEDVGSNKGAIIGLMGVVIATVITL 720
 QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOONGYENPTYKFFEQMON 770
 DB 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOONGYENPTYKFFEQMON 770
 RESULT 6
 US-08-464-250-3
 Sequence 3, Application US/08464250
 Patent No. 6300540
 GENERAL INFORMATION:
 APPLICANT: HARDY, John Anthony
 GOATE, Allison Mary
 MULLAN, Michael John
 CHARTIER-HARLIN, Marie-Christine
 OWEN, Michael John
 TITLE OF INVENTION: Test and Model for Alzheimer's Disease
 NUMBER OF SEQUENCES: 44
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourile and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,250
 FILING DATE: 05-Jun-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/104,165
 FILING DATE: 21-JAN-1992
 APPLICATION NUMBER: 9101307.8
 FILING DATE: 21-JAN-1991
 APPLICATION NUMBER: 9118445.7
 FILING DATE: 28-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Liebeschuetz, Joe
 REGISTRATION NUMBER: 37,505
 REFERENCE/DOCKET NUMBER: 16163-000100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 770 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-08-464-250-3
 Query Match 100.0%; Score 4058; DB 4; Length 770;
 Best Local Similarity 100.0%; Pred. No. 5.8e-281;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 61 TCIDTKEGIIQYCEVPELQITNVVEANQPVTIQNMCKRGRCKTHPHFVIRCLVG 120
 QY 121 EFVSDALLVPDKCFIHOERANDYCEHLLHHVYAKETCSKSTNLNDYGLMLRCGIDKFR 180
 DB 121 EFVSDALLVPDKCFIHOERANDYCEHLLHHVYAKETCSKSTNLNDYGLMLRCGIDKFR 180
 QY 181 GVEFVCCPLAEESDNDVSDADAEEDSDVMGADTDIADSEKVVVEAEVEAEVEE 240
 DB 181 GVEFVCCPLAEESDNDVSDADAEEDSDVMGADTDIADSEKVVVEAEVEAEVEE 240
 QY 241 EADDDDEDDGDEVEEAEPEYEATEERTSIATTTTTTTESEVEYREVCSQAEFGPC 300
 DB 241 EADDDDEDDGDEVEEAEPEYEATEERTSIATTTTTTTESEVEYREVCSQAEFGPC 300
 QY 301 RAMISRWYEDVTEGKCAFFYGGCGGGRNNFDTEYCMAYCGSAMQSLLKTTQEPILAD 360
 DB 301 RAMISRWYEDVTEGKCAFFYGGCGGGRNNFDTEYCMAYCGSAMQSLLKTTQEPILAD 360
 QY 361 PVKLPPTTAAPDAVDKYLETPGDENENHAFQAKERLEKHKRERSQVVRMEAEERQA 420
 DB 361 PVKLPPTTAAPDAVDKYLETPGDENENHAFQAKERLEKHKRERSQVVRMEAEERQA 420
 QY 421 KNLPRADKKAIVIOFOEYVESLBOEAEANERQQLVETHMARVEAMLNDRRLALENTYIAL 480
 DB 421 KNLPRADKKAIVIOFOEYVESLBOEAEANERQQLVETHMARVEAMLNDRRLALENTYIAL 480
 QY 481 QAVPRPRRHVFNMLKRYVRAEOKDRQHTLKHFEHVRVNDPKKAQIRSQVTHLRYIER 540
 DB 481 QAVPRPRRHVFNMLKRYVRAEOKDRQHTLKHFEHVRVNDPKKAQIRSQVTHLRYIER 540
 QY 541 MNOSLSILYVPAVEIIOEVDDELQKEONYSDVYANMISPRISYGDALMPSLTET 600
 DB 541 MNOSLSILYVPAVEIIOEVDDELQKEONYSDVYANMISPRISYGDALMPSLTET 600
 QY 601 KTTVELLPVNGEESLDLOQWHSFGADSVAPANTENEVEPYDARPADRGLTTRPGSLTN 660
 DB 601 KTTVELLPVNGEESLDLOQWHSFGADSVAPANTENEVEPYDARPADRGLTTRPGSLTN 660
 QY 661 IKTEEISEVMDAEFRHDSGEYVHOKLVFPAEDVGSNKGAIIGLMGVVIATVITL 720
 DB 661 IKTEEISEVMDAEFRHDSGEYVHOKLVFPAEDVGSNKGAIIGLMGVVIATVITL 720
 QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOONGYENPTYKFFEQMON 770
 DB 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOONGYENPTYKFFEQMON 770
 RESULT 7
 US-08-123-702-4
 Sequence 4, Application US/08123702
 Patent No. 5604131
 GENERAL INFORMATION:
 APPLICANT: Wadsworth, Samuel
 APPLICANT: Snyder, Benjamin
 APPLICANT: Reddy, Verma, B.
 TITLE OF INVENTION: A cDNA Genomic Hybrid Sequence Encoding App770
 Patent No. 5604131
 TITLE OF INVENTION: Containing a Genomic DNA Insert of the KI and OX-2 Regions
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Patricia L. Pabst
 STREET: 2800 One Atlantic Center
 STREET: 1201 West Peachtree Street
 CITY: Atlanta
 STATE: GA
 COUNTRY: USA
 ZIP: 30309-3450
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,702
FILING DATE: 17-SEPT-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Padst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: TS1121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-702-4

Query Match 97.2%; Score 3943.5; DB 1; Length 751;
Best Local Similarity 97.4%; Pred. No. 8e-273;
Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MLPGALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMYONKMSDPSGK 60
DB 1 MLPGALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMYONKMSDPSGK 60
QY 61 TCIDTKEGIIQCOEYVPELOITNVVEANOPVTIONMCKRGKCKTHPHFVIRCLVG 120
DB 61 TCIDTKEGIIQCOEYVPELOITNVVEANOPVTIONMCKRGKCKTHPHFVIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNDVSADAEEDSDVMWGADTDYADGSEDKVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAEESDNDVSADAEEDSDVMWGADTDYADGSEDKVVEAEVEAEVEE 240
QY 241 EADDDDEDEDEVEEAEPEATEERTTSIATTTTTTSVEEVVREVCSEAEFGPC 300
DB 241 EADDDDEDEDEVEEAEPEATEERTTSIATTTTTTSVEEVVREVCSEAEFGPC 300
QY 301 RAMISRWYFDVTEGKCAPFFGCGGNRNNDTEEYCAVGSAMSOSLKTQEPILARD 360
DB 301 RAMISRWYFDVTEGKCAPFFGCGGNRNNDTEEYCAVGSAMSOSLKTQEPILARD 360
QY 361 PVKLPTTAAPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVMREWEAEERQA 420
DB 361 PVKLPTTAAPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVMREWEAEERQA 420
QY 421 KNLPAKAKKAVIOHFOKVESLBOEANEEROQVLETHMARVEALNRRRLALENTYIAL 480
DB 421 KNLPAKAKKAVIOHFOKVESLBOEANEEROQVLETHMARVEALNRRRLALENTYIAL 480
QY 481 QAVPRPRHVFNMKKYVRAEQKDRQHTLKFHEHVRVMDPKKAQIISQVATHLRYER 540
DB 481 QAVPRPRHVFNMKKYVRAEQKDRQHTLKFHEHVRVMDPKKAQIISQVATHLRYER 540
QY 541 MNSLSLLVNPAAVEIODEVDELQKBOYSDVLANMISEPRISYGNDALMPSLET 600
DB 541 MNSLSLLVNPAAVEIODEVDELQKBOYSDVLANMISEPRISYGNDALMPSLET 600
QY 601 KTYVELLPVNGEFLDLOLPHSGADSVAPANTENEVEPDARAARGLTPRGSGSLTN 660
DB 601 KTYVELLPVNGEFLDLOLPHSGADSVAPANTENEVEPDARAARGLTPRGSGSLTN 660
QY 661 KTEELISEVMDAEFRHDSGEVHHQKLVFAEDVGSNKALIGIAMGVIAIVITL 720
DB 661 KTEELISEVMDAEFRHDSGEVHHQKLVFAEDVGSNKALIGIAMGVIAIVITL 720
QY 721 VMLKKQYTSIHGCVVEVDAVTPERHLSKMQONGYENPTYKFEEDQON 770
DB 721 VMLKKQYTSIHGCVVEVDAVTPERHLSKMQONGYENPTYKFEEDQON 770

Db 702 VMLKKQYTSIHGCVVEVDAVTPERHLSKMQONGYENPTYKFEEDQON 751

RESULT 8
US-08-104-165-2
Sequence 2, Application US/08104165
Patent No. 5877015
GENERAL INFORMATION:
APPLICANT: HARDY, John Anthony
APPLICANT: GOATE, Alison Mary
APPLICANT: MULLEN, Michael John
APPLICANT: CHARTIER-HARLIN, Marie-Christine
APPLICANT: OWEN, Michael John
TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/104,165
FILING DATE: 21-JAN-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16163-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-104-165-2

Query Match 97.2%; Score 3943.5; DB 2; Length 751;
Best Local Similarity 97.4%; Pred. No. 8e-273;
Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MLPGALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMYONKMSDPSGK 60
DB 1 MLPGALLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMYONKMSDPSGK 60
QY 61 TCIDTKEGIIQCOEYVPELOITNVVEANOPVTIONMCKRGKCKTHPHFVIRCLVG 120
DB 61 TCIDTKEGIIQCOEYVPELOITNVVEANOPVTIONMCKRGKCKTHPHFVIRCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMTVAKETCSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNDVSADAEEDSDVMWGADTDYADGSEDKVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAEESDNDVSADAEEDSDVMWGADTDYADGSEDKVVEAEVEAEVEE 240
QY 241 EADDDDEDEDEVEEAEPEATEERTTSIATTTTTTSVEEVVREVCSEAEFGPC 300
DB 241 EADDDDEDEDEVEEAEPEATEERTTSIATTTTTTSVEEVVREVCSEAEFGPC 300


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Db 241 EADDDDEDEGDEVEEAEPYEAERTSIAATTTTSESVEVREYCSQAEETGPC 300
QY 301 RAMISRWYFVTEGKCAFPFYGGCGGNRNFDTEEYCMAYCSAMSQSLKTTOEPLARD 360
Db 301 RAMISRWYFVTEGKCAFPFYGGCGGNRNFDTEEYCMAYCSA----- 344
QY 361 PVKLPTTAASPDAVDKYLETPGDENENAHFOKAKERLEAKHREMSQVNRWEAEARQA 420
Db 345 ---IPTTAASTPDAVDKYLETPGDENENAHFOKAKERLEAKHREMSQVNRWEAEARQA 401
QY 421 KNLPRKADKKAIVIOHFOKVESLDEAEANEKQOVLVETIMARVEALNDRRLALENTYITAL 480
Db 402 KNLPRKADKKAIVIOHFOKVESLDEAEANEKQOVLVETIMARVEALNDRRLALENTYITAL 461
QY 481 QAVPPRRHVFNMKKYVRAEOKDRQHTLKHFEHVRVADPKKAQIRSOVTHLRVIER 540
Db 462 QAVPPRRHVFNMKKYVRAEOKDRQHTLKHFEHVRVADPKKAQIRSOVTHLRVIER 521
QY 541 MNOSLSLLVNPVPAVEEIODEVDELLOKEQNSDDVLANNISEPRISYGDALMPSLJET 600
Db 522 MNOSLSLLVNPVPAVEEIODEVDELLOKEQNSDDVLANNISEPRISYGDALMPSLJET 581
QY 601 KTYVELLPVNGEESLDLOLQPMHSGADSVAPANTENEVEPYDARPAADRGILTTRPGSGLTN 660
Db 582 KTYVELLPVNGEESLDLOLQPMHSGADSVAPANTENEVEPYDARPAADRGILTTRPGSGLTN 641
QY 661 IKTEEISEVKMDAEFRHDSGVEVHHOKLVFEAEVGSNKGAIIGLAWGVVIAIVITL 720
Db 642 IKTEEISEVKMDAEFRHDSGVEVHHOKLVFEAEVGSNKGAIIGLAWGVVIAIVITL 701
QY 721 VMLKKQYTSIHGVEVNDAAVTPBEERHLSKMOONGYENPTYKFEEDOMN 770
Db 702 VMLKKQYTSIHGVEVNDAAVTPBEERHLSKMOONGYENPTYKFEEDOMN 751

RESULT 9
US-08-422-333-2
; Sequence 2, Application US/08422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
; TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View
; STATE: CA
; COUNTRY: USA
; ZIP: 94043
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422.333
; FILING DATE: 13-APR-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Shearer, Peter R.
; REGISTRATION NUMBER: 28,117
; REFERENCE/DOCKET NUMBER: 21900-28048.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 966-1550
; TELEFAX: (415) 968-2438
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 751 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```

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; MOLECULE TYPE: protein
US-08-422-333-2
Query Match 97.2%; Score 3943.5; DB 2; Length 751;
Best Local Similarity 97.4%; Pred. No. 8e-273;
Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MPEGLALLLAAVTARALEVPTGNGNGLAEPOIAPFCGGLNHNHVNQNKNSDPSPGK 60
Db 1 MPEGLALLLAAVTARALEVPTGNGNGLAEPOIAPFCGGLNHNHVNQNKNSDPSPGK 60
QY 61 TCIDTREGILOCOEYVPELOITNVVEANOPVITONCKRGKROCKTHPFIPIRCLVG 120
Db 61 TCIDTREGILOCOEYVPELOITNVVEANOPVITONCKRGKROCKTHPFIPIRCLVG 120
QY 121 EFSVDALLVDEKCKFLHOERMDVCEETHLHNTYAKETCSKSTNLADYMLPCGIDKFR 180
Db 121 EFSVDALLVDEKCKFLHOERMDVCEETHLHNTYAKETCSKSTNLADYMLPCGIDKFR 180
QY 181 GVEFVCCPLAESDNDVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
Db 181 GVEFVCCPLAESDNDVDSADAEEDSDVWVGADTDYADGSEDKVVEAEVEEVEE 240
QY 241 EADDDDEDEGDEVEEAEPYEAERTSIAATTTTSESVEVREYCSQAEETGPC 300
Db 241 EADDDDEDEGDEVEEAEPYEAERTSIAATTTTSESVEVREYCSQAEETGPC 300
QY 301 RAMISRWYFVTEGKCAFPFYGGCGGNRNFDTEEYCMAYCSAMSQSLKTTOEPLARD 360
Db 301 RAMISRWYFVTEGKCAFPFYGGCGGNRNFDTEEYCMAYCSA----- 344
QY 361 PVKLPTTAASPDAVDKYLETPGDENENAHFOKAKERLEAKHREMSQVNRWEAEARQA 420
Db 345 ---IPTTAASTPDAVDKYLETPGDENENAHFOKAKERLEAKHREMSQVNRWEAEARQA 401
QY 421 KNLPRKADKKAIVIOHFOKVESLDEAEANEKQOVLVETIMARVEALNDRRLALENTYITAL 480
Db 402 KNLPRKADKKAIVIOHFOKVESLDEAEANEKQOVLVETIMARVEALNDRRLALENTYITAL 461
QY 481 QAVPPRRHVFNMKKYVRAEOKDRQHTLKHFEHVRVADPKKAQIRSOVTHLRVIER 540
Db 462 QAVPPRRHVFNMKKYVRAEOKDRQHTLKHFEHVRVADPKKAQIRSOVTHLRVIER 521
QY 541 MNOSLSLLVNPVPAVEEIODEVDELLOKEQNSDDVLANNISEPRISYGDALMPSLJET 600
Db 522 MNOSLSLLVNPVPAVEEIODEVDELLOKEQNSDDVLANNISEPRISYGDALMPSLJET 581
QY 601 KTYVELLPVNGEESLDLOLQPMHSGADSVAPANTENEVEPYDARPAADRGILTTRPGSGLTN 660
Db 582 KTYVELLPVNGEESLDLOLQPMHSGADSVAPANTENEVEPYDARPAADRGILTTRPGSGLTN 641
QY 661 IKTEEISEVKMDAEFRHDSGVEVHHOKLVFEAEVGSNKGAIIGLAWGVVIAIVITL 720
Db 642 IKTEEISEVKMDAEFRHDSGVEVHHOKLVFEAEVGSNKGAIIGLAWGVVIAIVITL 701
QY 721 VMLKKQYTSIHGVEVNDAAVTPBEERHLSKMOONGYENPTYKFEEDOMN 770
Db 702 VMLKKQYTSIHGVEVNDAAVTPBEERHLSKMOONGYENPTYKFEEDOMN 751

RESULT 10
US-08-422-333-21
; Sequence 21, Application US/08422333
; Patent No. 5912410
; GENERAL INFORMATION:
; APPLICANT: CORDELL, Barbara L.
; TITLE OF INVENTION: TRANSGENIC NON-HUMAN MAMMAL DISPLAYING
; TITLE OF INVENTION: THE AMYLOID-FORMING PATHOLOGY OF ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scios, Inc.
; STREET: 2450 Bayshore Parkway
; CITY: Mountain View

```

STATE: CA
COUNTRY: USA
ZIP: 94043
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,333
FILING DATE: 13-APR-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Shearer, Peter R.
REGISTRATION NUMBER: 28,117
REFERENCE/DOCKET NUMBER: 21900-28048.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 966-1550
TELEFAX: (415) 968-2438
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-422-333-21

Query Match 97.28; Score 3943.5; DB 2; Length 751;
Best Local Similarity 97.48; Pred. No. 8e-273;
Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MLEPGLALLLAAMTARALEVPTDNGAGLLAEPQIAMFCGRLLNMHMYONKMDSPSGTK 60
DB 1 MLEPGLALLLAAMTARALEVPTDNGAGLLAEPQIAMFCGRLLNMHMYONKMDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANOPVTIONMCKRGKCKTHPFIYRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELOITNVVEANOPVTIONMCKRGKCKTHPFIYRCLVG 120
QY 121 EFVSDALLVPDKCKFLQERNDVCTHLHMTTAKETCSEKSTVLHDYGMILPGIDKFR 180
DB 121 EFVSDALLVPDKCKFLQERNDVCTHLHMTTAKETCSEKSTVLHDYGMILPGIDKFR 180
QY 121 EFVSDALLVPDKCKFLQERNDVCTHLHMTTAKETCSEKSTVLHDYGMILPGIDKFR 180
DB 121 EFVSDALLVPDKCKFLQERNDVCTHLHMTTAKETCSEKSTVLHDYGMILPGIDKFR 180
QY 181 GVEFVCCPLAESDNVNSADAEEDSDVMWGAIDTADGSEDDVVEAEVEEAEVEE 240
DB 181 GVEFVCCPLAESDNVNSADAEEDSDVMWGAIDTADGSEDDVVEAEVEEAEVEE 240
QY 241 EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTTSVEVEYREYCSQAETGPC 300
DB 241 EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTTSVEVEYREYCSQAETGPC 300
QY 241 EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTTSVEVEYREYCSQAETGPC 300
DB 241 EADDEDEDEGDEVEEAEPEYEATERTTSIATTTTTSVEVEYREYCSQAETGPC 300
QY 301 RAMISRYEPTVECKCAFFYGGGGGNNRNFDTREYCMAYCGSAMOSLKTTOEPLARD 360
DB 301 RAMISRYEPTVECKCAFFYGGGGGNNRNFDTREYCMAYCGSAMOSLKTTOEPLARD 360
QY 301 RAMISRYEPTVECKCAFFYGGGGGNNRNFDTREYCMAYCGSAMOSLKTTOEPLARD 360
DB 301 RAMISRYEPTVECKCAFFYGGGGGNNRNFDTREYCMAYCGSAMOSLKTTOEPLARD 360
QY 361 PVKLPFTAASPTDAVDYLETPTGDENEHAHOKAKERLEAKHRRMSQVHREWEAEROA 420
DB 361 PVKLPFTAASPTDAVDYLETPTGDENEHAHOKAKERLEAKHRRMSQVHREWEAEROA 420
QY 345 ---IPTTAASPTDAVDYLETPTGDENEHAHOKAKERLEAKHRRMSQVHREWEAEROA 401
DB 345 ---IPTTAASPTDAVDYLETPTGDENEHAHOKAKERLEAKHRRMSQVHREWEAEROA 401
QY 421 KNLPRKADKAVIQHFOEKVSELEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
DB 421 KNLPRKADKAVIQHFOEKVSELEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 480
QY 402 KNLPRKADKAVIQHFOEKVSELEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 461
DB 402 KNLPRKADKAVIQHFOEKVSELEQEAANERQOLVETHMARVEAMLNDRRLALENYITAL 461
QY 481 QAVPRRHRHFNMLKKVRAEQKROHTLKHFEHVRVNDPKKAQIISQVTHLRVIER 540
DB 481 QAVPRRHRHFNMLKKVRAEQKROHTLKHFEHVRVNDPKKAQIISQVTHLRVIER 540
QY 462 QAVPRRHRHFNMLKKVRAEQKROHTLKHFEHVRVNDPKKAQIISQVTHLRVIER 521
DB 462 QAVPRRHRHFNMLKKVRAEQKROHTLKHFEHVRVNDPKKAQIISQVTHLRVIER 521
QY 541 MNOSLILYVPAVAEETIODEVDELQEQNSDVLANNISEPRISYGDALPSTLET 600
DB 541 MNOSLILYVPAVAEETIODEVDELQEQNSDVLANNISEPRISYGDALPSTLET 600
QY 522 MNOSLILYVPAVAEETIODEVDELQEQNSDVLANNISEPRISYGDALPSTLET 581
DB 522 MNOSLILYVPAVAEETIODEVDELQEQNSDVLANNISEPRISYGDALPSTLET 581
QY 601 KTVVELLPVNGEESLDDLOPMHSGADSVPAANTEVEPYDARPAADRGILTRPGSLTN 660
DB 601 KTVVELLPVNGEESLDDLOPMHSGADSVPAANTEVEPYDARPAADRGILTRPGSLTN 660

DB 582 KTVVELLPVNGEESLDDLOPMHSGADSVPAANTEVEPYDARPAADRGILTRPGSLTN 641
QY 661 IKTEEISEVMDAEFRDSDGVYHHOKLVFAEDVGSNKAGIIGMVGVIATVIYITL 720
DB 642 IKTEEISEVMDAEFRDSDGVYHHOKLVFAEDVGSNKAGIIGMVGVIATVIYITL 701
QY 721 VMLKKKQYTSIHGQVVEVDAVAPPEERHLSKMOONGYENPTYKFEEDOMON 770
DB 702 VMLKKKQYTSIHGQVVEVDAVAPPEERHLSKMOONGYENPTYKFEEDOMON 751

RESULT 11

US-08-464-250-2
Sequence 2, Application US/08464250
Patent No. 6107542
GENERAL INFORMATION:
APPLICANT: HARDY, John Anthony
APPLICANT: GOATE, Allison Mary
APPLICANT: MULLAN, Michael John
APPLICANT: CHARTIER-HARLIN, Marie-Christine
APPLICANT: OWEN, Michael John
TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Knourle and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,250
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/104,165
FILING DATE: 21-JAN-1992
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16163-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-250-2

Query Match 97.28; Score 3943.5; DB 3; Length 751;
Best Local Similarity 97.48; Pred. No. 8e-273;
Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MLEPGLALLLAAMTARALEVPTDNGAGLLAEPQIAMFCGRLLNMHMYONKMDSPSGTK 60
DB 1 MLEPGLALLLAAMTARALEVPTDNGAGLLAEPQIAMFCGRLLNMHMYONKMDSPSGTK 60
QY 61 TCIDTKEGILQYCOEYVPELOITNVVEANOPVTIONMCKRGKCKTHPFIYRCLVG 120
DB 61 TCIDTKEGILQYCOEYVPELOITNVVEANOPVTIONMCKRGKCKTHPFIYRCLVG 120

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QY 121 EFVSDALLVPDKCKFLHOERNDVCETHLHHTVAKETCSKSTNLDHYGMLPCGIDKFR 180
    |||
DB 121 EFVSDALLVPDKCKFLHOERNDVCETHLHHTVAKETCSKSTNLDHYGMLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVSADAEEEDSDVMWGADTDYADGSEDKVVEAEVEEAEVEE 240
    |||
DB 181 GVEFVCCPLAEESDNVSADAEEEDSDVMWGADTDYADGSEDKVVEAEVEEAEVEE 240
QY 241 EADDEDEDEGDEVEEAEERPEATERTTSIATTTTTTSEVEVREVCSQAETGPC 300
    |||
DB 241 EADDEDEDEGDEVEEAEERPEATERTTSIATTTTTTSEVEVREVCSQAETGPC 300
QY 241 EADDEDEDEGDEVEEAEERPEATERTTSIATTTTTTSEVEVREVCSQAETGPC 300
    |||
DB 241 EADDEDEDEGDEVEEAEERPEATERTTSIATTTTTTSEVEVREVCSQAETGPC 300
QY 301 RAMISRMVFDVTEGKCAPFEYGGCGGNRNFDTEYCAVCGSA----- 344
    |||
DB 301 RAMISRMVFDVTEGKCAPFEYGGCGGNRNFDTEYCAVCGSA----- 344
QY 361 PVKLPPTAASPDAVDKYLETTPGDENEHAHFOKAKERLEAKHRRMSQVMREWEAEERQA 420
    |||
DB 361 PVKLPPTAASPDAVDKYLETTPGDENEHAHFOKAKERLEAKHRRMSQVMREWEAEERQA 420
QY 345 ---IPTTAASPDAVDKYLETTPGDENEHAHFOKAKERLEAKHRRMSQVMREWEAEERQA 401
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DB 345 ---IPTTAASPDAVDKYLETTPGDENEHAHFOKAKERLEAKHRRMSQVMREWEAEERQA 401
QY 421 KNLPRKADKAVIOHFOEKVESLEOEANERQOLVETHMARVEAMLNDRRLALENYITAL 480
    |||
DB 421 KNLPRKADKAVIOHFOEKVESLEOEANERQOLVETHMARVEAMLNDRRLALENYITAL 480
QY 402 KNLPRKADKAVIOHFOEKVESLEOEANERQOLVETHMARVEAMLNDRRLALENYITAL 461
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DB 402 KNLPRKADKAVIOHFOEKVESLEOEANERQOLVETHMARVEAMLNDRRLALENYITAL 461
QY 481 QAVPRPRHVFNMKKYVRABOKROHTLKFHEHVRWVDPKKAQIISQVWTHLRVIYER 540
    |||
DB 481 QAVPRPRHVFNMKKYVRABOKROHTLKFHEHVRWVDPKKAQIISQVWTHLRVIYER 540
QY 462 QAVPRPRHVFNMKKYVRABOKROHTLKFHEHVRWVDPKKAQIISQVWTHLRVIYER 521
    |||
DB 462 QAVPRPRHVFNMKKYVRABOKROHTLKFHEHVRWVDPKKAQIISQVWTHLRVIYER 521
QY 541 MNOSSLILYNPAVAEETODEVDELQEKONYSDVLANMISEPRISYGNALMPSLLET 600
    |||
DB 541 MNOSSLILYNPAVAEETODEVDELQEKONYSDVLANMISEPRISYGNALMPSLLET 600
QY 522 MNOSSLILYNPAVAEETODEVDELQEKONYSDVLANMISEPRISYGNALMPSLLET 581
    |||
DB 522 MNOSSLILYNPAVAEETODEVDELQEKONYSDVLANMISEPRISYGNALMPSLLET 581
QY 601 KTYVELLPVNGEESLIDLQPHWSFGADSVPAANTEVEVPVADRAPADRGTLTRGSGLTN 660
    |||
DB 601 KTYVELLPVNGEESLIDLQPHWSFGADSVPAANTEVEVPVADRAPADRGTLTRGSGLTN 660
QY 661 KTYVELLPVNGEESLIDLQPHWSFGADSVPAANTEVEVPVADRAPADRGTLTRGSGLTN 720
    |||
DB 661 KTYVELLPVNGEESLIDLQPHWSFGADSVPAANTEVEVPVADRAPADRGTLTRGSGLTN 720
QY 642 IKTEEISEVKMDAFRRDSGVEVHOKLVFAEYVGSNKGAIIGLMGGVIAIVYITL 701
    |||
DB 642 IKTEEISEVKMDAFRRDSGVEVHOKLVFAEYVGSNKGAIIGLMGGVIAIVYITL 701
QY 721 VMLKKKQYTSIHGVEVEYDAVTPPEERHLSKMOONGYENPTYKFEFQMON 770
    |||
DB 721 VMLKKKQYTSIHGVEVEYDAVTPPEERHLSKMOONGYENPTYKFEFQMON 770
QY 702 VMLKKKQYTSIHGVEVEYDAVTPPEERHLSKMOONGYENPTYKFEFQMON 751
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DB 702 VMLKKKQYTSIHGVEVEYDAVTPPEERHLSKMOONGYENPTYKFEFQMON 751

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RESULT 12
US-08-464-250-2
Sequence 2, Application US/08464250
Patent No. 6300540

GENERAL INFORMATION:

APPLICANT: HARDY, John Anthony
GOATE, Allison Mary
MULLEN, Michael John
CHARTIER-HARLIN, Marie-Christine
OWEN, Michael John
TITLE OF INVENTION: Test and Model for Alzheimer's Disease
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,250
FILING DATE: 05-Jun-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

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APPLICATION NUMBER: 08/104,165
FILING DATE: 21-JAN-1992
APPLICATION NUMBER: 9101307.8
FILING DATE: 21-JAN-1991
APPLICATION NUMBER: 9118445.7
FILING DATE: 28-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liedschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 16163-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 751 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-464-250-2

Query Match          97.2%; Score 3943.5; DB 4; Length 751;
Best Local Similarity 97.4%; Pred. No. 8e-273;
Matches 730; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MLEPGLALLLAAWTAARALEVPTDGNAGLAEPOIAMECGRLNMHMNVQNGKWDSPSGTK 60
DB 1 MLEPGLALLLAAWTAARALEVPTDGNAGLAEPOIAMECGRLNMHMNVQNGKWDSPSGTK 60
QY 61 TCIDTKGIGIYOCEVYRPELQITNVVANOPVTQNMCKRGKCKTHPHVITRYCLVG 120
DB 61 TCIDTKGIGIYOCEVYRPELQITNVVANOPVTQNMCKRGKCKTHPHVITRYCLVG 120
QY 121 EFVSDALLVPDKCKFLHOERNDVCETHLHHTVAKETCSKSTNLDHYGMLPCGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERNDVCETHLHHTVAKETCSKSTNLDHYGMLPCGIDKFR 180
QY 181 GVEFVCCPLAEESDNVSADAEEEDSDVMWGADTDYADGSEDKVVEAEVEEAEVEE 240
DB 181 GVEFVCCPLAEESDNVSADAEEEDSDVMWGADTDYADGSEDKVVEAEVEEAEVEE 240
QY 241 EADDEDEDEGDEVEEAEERPEATERTTSIATTTTTTSEVEVREVCSQAETGPC 300
DB 241 EADDEDEDEGDEVEEAEERPEATERTTSIATTTTTTSEVEVREVCSQAETGPC 300
QY 301 RAMISRMVFDVTEGKCAPFEYGGCGGNRNFDTEYCAVCGSAMOSLSLKTQEPRLARD 360
DB 301 RAMISRMVFDVTEGKCAPFEYGGCGGNRNFDTEYCAVCGSAMOSLSLKTQEPRLARD 360
QY 361 PVKLPPTAASPDAVDKYLETTPGDENEHAHFOKAKERLEAKHRRMSQVMREWEAEERQA 420
DB 361 PVKLPPTAASPDAVDKYLETTPGDENEHAHFOKAKERLEAKHRRMSQVMREWEAEERQA 420
QY 345 ---IPTTAASPDAVDKYLETTPGDENEHAHFOKAKERLEAKHRRMSQVMREWEAEERQA 401
DB 345 ---IPTTAASPDAVDKYLETTPGDENEHAHFOKAKERLEAKHRRMSQVMREWEAEERQA 401
QY 421 KNLPRKADKAVIOHFOEKVESLEOEANERQOLVETHMARVEAMLNDRRLALENYITAL 480
DB 421 KNLPRKADKAVIOHFOEKVESLEOEANERQOLVETHMARVEAMLNDRRLALENYITAL 480
QY 402 KNLPRKADKAVIOHFOEKVESLEOEANERQOLVETHMARVEAMLNDRRLALENYITAL 461
DB 402 KNLPRKADKAVIOHFOEKVESLEOEANERQOLVETHMARVEAMLNDRRLALENYITAL 461
QY 481 QAVPRPRHVFNMKKYVRABOKROHTLKFHEHVRWVDPKKAQIISQVWTHLRVIYER 540
DB 481 QAVPRPRHVFNMKKYVRABOKROHTLKFHEHVRWVDPKKAQIISQVWTHLRVIYER 540
QY 462 QAVPRPRHVFNMKKYVRABOKROHTLKFHEHVRWVDPKKAQIISQVWTHLRVIYER 521
DB 462 QAVPRPRHVFNMKKYVRABOKROHTLKFHEHVRWVDPKKAQIISQVWTHLRVIYER 521
QY 541 MNOSSLILYNPAVAEETODEVDELQEKONYSDVLANMISEPRISYGNALMPSLLET 600
DB 541 MNOSSLILYNPAVAEETODEVDELQEKONYSDVLANMISEPRISYGNALMPSLLET 600
QY 522 MNOSSLILYNPAVAEETODEVDELQEKONYSDVLANMISEPRISYGNALMPSLLET 581
DB 522 MNOSSLILYNPAVAEETODEVDELQEKONYSDVLANMISEPRISYGNALMPSLLET 581
QY 601 KTYVELLPVNGEESLIDLQPHWSFGADSVPAANTEVEVPVADRAPADRGTLTRGSGLTN 660
DB 601 KTYVELLPVNGEESLIDLQPHWSFGADSVPAANTEVEVPVADRAPADRGTLTRGSGLTN 660
QY 582 KTYVELLPVNGEESLIDLQPHWSFGADSVPAANTEVEVPVADRAPADRGTLTRGSGLTN 641
DB 582 KTYVELLPVNGEESLIDLQPHWSFGADSVPAANTEVEVPVADRAPADRGTLTRGSGLTN 641
QY 661 IKTEEISEVKMDAFRRDSGVEVHOKLVFAEYVGSNKGAIIGLMGGVIAIVYITL 720
DB 661 IKTEEISEVKMDAFRRDSGVEVHOKLVFAEYVGSNKGAIIGLMGGVIAIVYITL 720

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Db 642 KTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKAIGLMVGSVIATVITL 701
QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEQMON 770
Db 702 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEQMON 751
RESULT 13
5187153-2
Patent No. 5187153
APPLICANT: CORDELL, BARBARA; SCHILLING, JAMES W.; KATUNOMA, NOBUHIKO
TITLE OF INVENTION: METHODS OF TREATMENT USING ALZHEIMER'S
AMYLOID POLYPEPTIDE DERIVATIVES
NUMBER OF SEQUENCES: 33
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/502,273
FILING DATE: 29-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 361,912
FILING DATE: 06-JUN-1989
APPLICATION NUMBER: 359,911
FILING DATE: 12-MAY-1989
APPLICATION NUMBER: 87,002
FILING DATE: 18-AUG-1987
APPLICATION NUMBER: 8,810
FILING DATE: 30-JAN-1987
APPLICATION NUMBER: 948,376
FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
FILING DATE: 17-NOV-1986
SEQ ID NO: 2:
LENGTH: 751
5187153-2

Query Match 97.28; Score 3943.5; DB 6; Length 751;
Best Local Similarity 97.48; Pred. No. 8e-273;
Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MLPGLALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRIMHNNYONGKMDSPSGTK 60
Db 1 MLPGLALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRIMHNNYONGKMDSPSGTK 60
QY 61 TCIDTKEGIILOYCOEYVPELOITNVVEANOPVTIONMCKRGRKOCKTHPHFVPIRYCLVG 120
Db 61 TCIDTKEGIILOYCOEYVPELOITNVVEANOPVTIONMCKRGRKOCKTHPHFVPIRYCLVG 120
QY 121 EFVSALLVPKCKFLHDERMDVCEHLHMTVAKETCSEKSTNLHDYGMLLPGSIDKFR 180
Db 121 EFVSALLVPKCKFLHDERMDVCEHLHMTVAKETCSEKSTNLHDYGMLLPGSIDKFR 180
QY 181 GVEFVCCPLAEBSNVDSADAEEEDSDVWVGADTDYADGSEDKVVEAAEEVEAAVEEE 240
Db 181 GVEFVCCPLAEBSNVDSADAEEEDSDVWVGADTDYADGSEDKVVEAAEEVEAAVEEE 240
QY 241 EADDEDEDEDGEVEEAEEPEYEATERTTSIATTTTTSVEEVEVREVCSEQAETGPC 300
Db 241 EADDEDEDEDGEVEEAEEPEYEATERTTSIATTTTTSVEEVEVREVCSEQAETGPC 300
QY 301 RAMTSRWTFDTEGKCAFEFGGCGGNRNNPDTREYCAVCGSAMSSOLKTQOPLARD 360
Db 301 RAMTSRWTFDTEGKCAFEFGGCGGNRNNPDTREYCAVCGSAMSSOLKTQOPLARD 360
QY 361 PVKLPTTAASTPDADVKTLETTPGDENEHAHFQAKERLEAKHRRMSQVMEAEAEQA 420
Db 361 PVKLPTTAASTPDADVKTLETTPGDENEHAHFQAKERLEAKHRRMSQVMEAEAEQA 420
QY 421 KNLPRADKKAIVIOHFOEKVESLEDEANERQOLVETHNARYEAMLNDRRRLALENYITAL 480
Db 421 KNLPRADKKAIVIOHFOEKVESLEDEANERQOLVETHNARYEAMLNDRRRLALENYITAL 480
QY 481 QAVPRPRHVNMLKKYVRAEQKDQHTLKHFEHVRMDPKKAQIRSOVMTHLRYIER 540
Db 481 QAVPRPRHVNMLKKYVRAEQKDQHTLKHFEHVRMDPKKAQIRSOVMTHLRYIER 540
QY 521 QAVPRPRHVNMLKKYVRAEQKDQHTLKHFEHVRMDPKKAQIRSOVMTHLRYIER 521
Db 521 QAVPRPRHVNMLKKYVRAEQKDQHTLKHFEHVRMDPKKAQIRSOVMTHLRYIER 521

QY 541 MNOSLILYNPAVAEEIODEVDELLOKEONYSDOVLAMTISEPRISYGNALMPSLJET 600
Db 522 MNOSLILYNPAVAEEIODEVDELLOKEONYSDOVLAMTISEPRISYGNALMPSLJET 581
QY 601 KTVLELVPNGEESLDDLOPHMSFGADSVPANTENEPVDPARAADGLTTRPGSGLTN 660
Db 582 KTVLELVPNGEESLDDLOPHMSFGADSVPANTENEPVDPARAADGLTTRPGSGLTN 641
QY 661 KTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKAIGLMVGSVIATVITL 720
Db 642 KTEEISEVKMDAEFRHDSGYEVHHQKLVFFAEDVGSNKAIGLMVGSVIATVITL 701
QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEQMON 770
Db 702 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQONGYENPTYKFEQMON 751

RESULT 14
5223482-2
Patent No. 5223482
APPLICANT: SCHILLING, JAMES W.; PONTE, PHYLLIS A.; CORDELL, BARBARA
TITLE OF INVENTION: RECOMBINANT ALZHEIMER'S PROTEASE
INHIBITORY AMYLOID PROTEIN AND METHOD OF USE
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/361,912
FILING DATE: 06-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 359,911
FILING DATE: 12-MAY-1989
APPLICATION NUMBER: 87,002
FILING DATE: 18-AUG-1987
APPLICATION NUMBER: 8,810
FILING DATE: 30-JAN-1987
APPLICATION NUMBER: 948,376
FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
FILING DATE: 17-NOV-1986
SEQ ID NO: 2:
LENGTH: 751
5223482-2

Query Match 97.28; Score 3943.5; DB 6; Length 751;
Best Local Similarity 97.48; Pred. No. 8e-273;
Matches 750; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

QY 1 MLPGLALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRIMHNNYONGKMDSPSGTK 60
Db 1 MLPGLALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRIMHNNYONGKMDSPSGTK 60
QY 61 TCIDTKEGIILOYCOEYVPELOITNVVEANOPVTIONMCKRGRKOCKTHPHFVPIRYCLVG 120
Db 61 TCIDTKEGIILOYCOEYVPELOITNVVEANOPVTIONMCKRGRKOCKTHPHFVPIRYCLVG 120
QY 121 EFVSALLVPKCKFLHDERMDVCEHLHMTVAKETCSEKSTNLHDYGMLLPGSIDKFR 180
Db 121 EFVSALLVPKCKFLHDERMDVCEHLHMTVAKETCSEKSTNLHDYGMLLPGSIDKFR 180
QY 181 GVEFVCCPLAEBSNVDSADAEEEDSDVWVGADTDYADGSEDKVVEAAEEVEAAVEEE 240
Db 181 GVEFVCCPLAEBSNVDSADAEEEDSDVWVGADTDYADGSEDKVVEAAEEVEAAVEEE 240
QY 241 EADDEDEDEDGEVEEAEEPEYEATERTTSIATTTTTSVEEVEVREVCSEQAETGPC 300
Db 241 EADDEDEDEDGEVEEAEEPEYEATERTTSIATTTTTSVEEVEVREVCSEQAETGPC 300
QY 301 RAMTSRWTFDTEGKCAFEFGGCGGNRNNPDTREYCAVCGSAMSSOLKTQOPLARD 360
Db 301 RAMTSRWTFDTEGKCAFEFGGCGGNRNNPDTREYCAVCGSAMSSOLKTQOPLARD 360
QY 361 PVKLPTTAASTPDADVKTLETTPGDENEHAHFQAKERLEAKHRRMSQVMEAEAEQA 420
Db 361 PVKLPTTAASTPDADVKTLETTPGDENEHAHFQAKERLEAKHRRMSQVMEAEAEQA 420

Db 345 ---IPTRASTPDVNDKLTETPGDENEHAFQKAKERLEAHRERMSQVMEBEAERQA 401
QY 421 KNLPRADKAVIOHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRRLALENYITAL 480
Db 402 KNLPRADKAVIOHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRRLALENYITAL 461
QY 481 QAVPPRRHVNMLKKYVRAEQKDRQHTLKFEHVRVDPKKAQIRSQVTHLRVIER 540
Db 462 QAVPPRRHVNMLKKYVRAEQKDRQHTLKFEHVRVDPKKAQIRSQVTHLRVIER 521
QY 541 MNOSLILYNPAVAEEIODEVDELLOKEQNSDDVLNMTSEPRISYGNALMPSLET 600
Db 522 MNOSLILYNPAVAEEIODEVDELLOKEQNSDDVLNMTSEPRISYGNALMPSLET 581
QY 601 KTYVELLPVNGEFSLDDLOPMHSGADSVPAANTENEVEPVADARPAADRGLTTRPGSLTN 660
Db 582 KTYVELLPVNGEFSLDDLOPMHSGADSVPAANTENEVEPVADARPAADRGLTTRPGSLTN 641
QY 661 IKTEISSEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIGLMGVVIAIVITL 720
Db 642 IKTEISSEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIGLMGVVIAIVITL 701
QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOONGYENPTYKFEPEOMON 770
Db 702 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOONGYENPTYKFEPEOMON 751

RESULT 15
5220013-2
PATENT No. 5220013
APPLICANT: PONTE, PHYLLIS A.; CORDELL, BARBARA
TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE DETECTION
OF ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/444,118
FILING DATE: 30-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 87,002
FILING DATE: 18-AUG-1987
APPLICATION NUMBER: 8,810
FILING DATE: 30-JAN-1987
APPLICATION NUMBER: 948,376
FILING DATE: 31-DEC-1986
APPLICATION NUMBER: 932,193
FILING DATE: 17-NOV-1986
SEQ ID NO: 2:
LENGTH: 751
5220013-2

Query Match 97.0%; Score 3937.5; DB 6; Length 751;
Best Local Similarity 97.1%; Pred. No. 2.1e-272;
Matches 748; Conservative 3; Mismatches 0; Indels 19; Gaps 1;

Db 241 EADDEDEDEGDEVEEAEEPEATEERTTSIATTTTTTSEVEVREVCSEQAETGPC 300
QY 301 RAMISRWTFDVTBEKCAPFFGGCGGNRNNDTEYCAVAGSAMOSLTTQOEPLARD 360
Db 301 RAMISRWTFDVTBEKCAPFFGGCGGNRNNDTEYCAVAGSAMOSLTTQOEPLARD 344
QY 361 PVKLPTASTPDVNDKLTETPGDENEHAFQKAKERLEAHRERMSQVMEBEAERQA 420
Db 345 ---IPTRASTPDVNDKLTETPGDENEHAFQKAKERLEAHRERMSQVMEBEAERQA 401
QY 421 KNLPRADKAVIOHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRRLALENYITAL 480
Db 402 KNLPRADKAVIOHFOEKVESLEQEAANERQOLVETHMARVEAMLNDRRRLALENYITAL 461
QY 481 QAVPPRRHVNMLKKYVRAEQKDRQHTLKFEHVRVDPKKAQIRSQVTHLRVIER 540
Db 462 QAVPPRRHVNMLKKYVRAEQKDRQHTLKFEHVRVDPKKAQIRSQVTHLRVIER 521
QY 541 MNOSLILYNPAVAEEIODEVDELLOKEQNSDDVLNMTSEPRISYGNALMPSLET 600
Db 522 MNOSLILYNPAVAEEIODEVDELLOKEQNSDDVLNMTSEPRISYGNALMPSLET 581
QY 601 KTYVELLPVNGEFSLDDLOPMHSGADSVPAANTENEVEPVADARPAADRGLTTRPGSLTN 660
Db 582 KTYVELLPVNGEFSLDDLOPMHSGADSVPAANTENEVEPVADARPAADRGLTTRPGSLTN 641
QY 661 IKTEISSEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIGLMGVVIAIVITL 720
Db 642 IKTEISSEVKMDAEFRHDSGYEVHHQKLVFAEDVGSNKGAIGLMGVVIAIVITL 701
QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOONGYENPTYKFEPEOMON 770
Db 702 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOONGYENPTYKFEPEOMON 751

Search completed: October 31, 2002, 10:13:33
Job time : 24.8364 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:56 ; Search time 30.3075 Seconds
(without alignments)
2441.270 Million cell updates/sec

Title: US-09-785-215-2
Perfect score: 4058

Sequence: 1 MREGALLLLAAMTARALEV.....KMQONGYENPTKFFEQMON 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.71.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
5: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4058	100.0	770	1	ORHDA4
2	3590.5	88.5	695	1	Alzheimer's diseases
3	3493.5	86.1	695	2	Alzheimer's diseases
4	3468.5	85.5	695	2	Alzheimer's diseases
5	3403.5	83.9	747	2	Alzheimer's diseases
6	2446.5	60.3	484	4	Alzheimer's diseases
7	1981.5	48.8	763	2	Alzheimer's diseases
8	1971.5	48.6	765	2	Alzheimer's diseases
9	1956.5	48.2	751	2	Alzheimer's diseases
10	1150.5	28.4	653	2	Alzheimer's diseases
11	1132.5	27.4	511	2	Alzheimer's diseases
12	785	19.3	686	2	Alzheimer's diseases
13	737.5	18.2	886	2	Alzheimer's diseases
14	706	17.4	246	2	Alzheimer's diseases
15	501	12.3	100	2	Alzheimer's diseases
16	411	10.1	82	2	Alzheimer's diseases
17	403	9.9	76	2	Alzheimer's diseases
18	397	9.8	76	2	Alzheimer's diseases
19	383	9.4	76	2	Alzheimer's diseases
20	296.5	7.3	191	2	Alzheimer's diseases
21	283	7.0	57	2	Alzheimer's diseases
22	283	7.0	57	2	Alzheimer's diseases
23	283	7.0	57	2	Alzheimer's diseases
24	283	7.0	57	2	Alzheimer's diseases
25	283	7.0	57	2	Alzheimer's diseases
26	283	7.0	57	2	Alzheimer's diseases
27	256.5	6.3	111	2	Alzheimer's diseases
28	217	5.3	42	2	Alzheimer's diseases
29	194.5	4.8	2225	2	Alzheimer's diseases

30	186	4.6	993	2	S49461	synaptonemal compl
31	183.5	4.5	396	2	S53325	tissue factor path
32	183	4.5	1188	2	T46608	zinc finger protei
33	179.5	4.4	1208	2	T27822	hypothetical prote
34	178.5	4.4	1110	2	S51116	NF-180 - sea lamp
35	177.5	4.4	2167	2	T34395	hypothetical prote
36	176.5	4.3	252	2	JG0185	hepatocyte growth
37	176	4.3	555	2	S30332	proteinase inhibit
38	175.5	4.3	579	2	JH0820	160K golgi antigen
39	175	4.3	302	1	T1RTGK	tissue factor path
40	175	4.3	1182	2	T30189	myelin transcriptpt
41	174.5	4.3	1271	2	A45555	glutamate rich pro
42	173.5	4.3	1087	2	T30330	gelsoatin-related p
43	173.5	4.3	1558	2	C89114	protein C37c3.6a l
44	172	4.2	922	2	T23573	hypothetical prote
45	170.5	4.2	5170	2	T15348	hypothetical prote

ALIGNMENTS

RESULT 1

ORHDA4

Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xla inl
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vasc
protein precursor splice form APP(770)

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1987 #sequence-revision 28-Jul-1995 #text-change 15-Sep-2000

C:Accession: S02260; S05194; A32277; A33260; A3486; I39452; I39451; I39453; I59562;

4668; A28583; A29302; A60805; JI0038; S06121; A60355; A59011; A33384; S29076; S38252;

R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;

Nucleic Acids Res. 17, 517-522, 1989

A:Title: The Pread(695) precursor protein of Alzheimer's disease A4 amyloid is encode

A:Reference number: S02260; MUID:89128427

A:Accession: S02260

A:Molecule type: DNA

A:Residues: 1-288, 'V', 365-770 <LEW1>

A:Cross-references: EMBL:X13466

A:Note: alternative splice form APP(695)

R:Lemaire, H.G.

submitted to the EMBL Data Library, November 1988

A:Reference number: S05194

A:Accession: S05194

A:Molecule type: DNA

A:Residues: 1-14, 'VM', 17-288, 'V', 365-770 <LEW2>

A:Cross-references: EMBL:X13466; NID:935598; PIDN:CAA31830.1; PID:9871360

A:Note: alternative splice form APP(695)

R:La Fautel, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.

Biochem. Biophys. Res. Commun. 159, 297-304, 1989

A:Title: Characterization of the 5'-end region and the first two exons of the beta-p

A:Reference number: A32277; MUID:89165870

A:Accession: A32277

A:Molecule type: DNA

A:Residues: 1-75 <LAF>

A:Cross-references: GB:M24546; GB:M24547; NID:9341202; PIDN:AAAC13654.1; PID:9516074

R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.

Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989

A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows siml

A:Reference number: A33260; MUID:89392030

A:Accession: A33260

A:Molecule type: DNA

A:Residues: 656-737 <JOH>

A:Cross-references: GB:M29270; NID:9178863; PIDN:AAAS1768.1; PID:9178865

R:Prelli, F.; Levy, E.; Van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, J

Biochem. Biophys. Res. Commun. 170, 301-307, 1990

A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid

A:Reference number: A35486; MUID:90321244

A:Accession: A35486

A:Molecule type: DNA

A:Residues: 672-710 <PREI>

A:Note: 693-Gln was found in DNA isolated from HCMA-D patients

R:Yoshikawa, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.

Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: 139451; MUID:90236318
 A:Accession: 139452
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M33112; NID:g178613; PIDN:AB59502.1; PID:g178616
 A:Accession: 139451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
 A:Molecule type: DNA
 A:Residues: 1-530, 'OMMPYPAFWFAKVG' <YOS2>
 A:Cross-references: GB:M34875; NID:g178608; PIDN:AB59501.1; PID:g178615
 R:Yoshitani, S.I.; Sasaki, H.; Dohura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168
 A:Contents: annotation; erratum
 A:Note: revised physical map for reference 139451
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrhage 248, 1124-1126, 1990
 A:Accession: 139453; MUID:90260663
 A:Reference number: 139453
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:g178618; PIDN:AA51727.1; PID:g178620
 A:Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer's disease
 A:Reference number: 159562; MUID:9022553
 A:Accession: 159562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'F', 718-737 <MUR>
 A:Accession: 159562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'F', 718-737 <MUR>
 A:Cross-references: GB:S57665; NID:g236720; PIDN:AB19991.1; PID:g236721
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wajsbman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson, A.; J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
 A:Reference number: A44017; MUID:93035397
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692, 'G', 694-718 <KAM1>
 A:Cross-references: GB:S45135; NID:g257377; PIDN:AB23645.1; PID:g257378
 A:Experimental source: Familial Alzheimer disease family SB
 A:Note: sequence extracted from NCBI backbone (NCBI:115374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <KAM2>
 A:Cross-references: GB:S45136; NID:g257379; PIDN:AB23646.1; PID:g257380
 A:Experimental source: Familial Alzheimer disease family LT
 A:Note: sequence extracted from NCBI backbone (NCBI:115376)
 A:Note: this sequence has a silent mutation
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grieschik, K.H.; Nature 325, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
 A:Reference number: A03134; MUID:87144572
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAN>
 A:Cross-references: GB:Y00264; NID:g28525; PIDN:CA68374.1; PID:g28526
 A:Note: alternative splice form APP(695)
 R:Robak, N.K.; Ramakrishna, N.; Wolte, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular A
 A:Reference number: A29030; MUID:87231971
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A:Cross-references: GB:M16765; NID:g178539; PIDN:AA51722.1; PID:g178540
 A:Note: the authors translated the codon GAG for residue 647 as Asp

R:Goldhaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A:Title: Characterization and chromosomal localization of a cDNA encoding brain amylo
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', 758-770 <GOL>
 A:Cross-references: GB:M15533; NID:g178706; PIDN:AA35540.1; PID:g178707
 A:Experimental source: Brain
 R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van
 Science 235, 880-884, 1987
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near
 A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TAN1>
 A:Cross-references: GB:M15532; NID:g177957; PIDN:AA51564.1; PID:g177958
 R:Dykes, T.; Weidmann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue
 EMBO J. 7, 949-957, 1988
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 p
 A:Reference number: 502638; MUID:88296437
 A:Accession: 502638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DYR>
 R:Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; N
 Nature 331, 528-530, 1988
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc
 A:Reference number: 500707; MUID:88122640
 A:Accession: 500707
 A:Molecule type: mRNA
 A:Residues: 286-344, 'I', 365-366 <TAN2>
 A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CA30042.1; PID:g2929612
 A:Experimental source: promyelocytic leukemia cell line HL60
 R:Ponte, P.; Gonzalez-Dewhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;
 Nature 331, 525-527, 1988
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inh
 A:Reference number: 500925; MUID:88122639
 A:Accession: 500925
 A:Molecule type: mRNA
 A:Residues: 1-344, 'I', 365-770 <PO2>
 A:Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CA30050.1; PID:g28721
 A:Note: alternative splice form APP(770)
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi
 A:Reference number: A38949; MUID:88122641
 A:Accession: A38949
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>
 A:Cross-references: GB:X06981; NID:g28816; PIDN:CA30041.1; PID:g929611
 A:Experimental source: glioblastoma cell line
 A:Note: alternative splice form APP(770)
 R:Vitek, M.P.; Rasooli, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre
 A:Reference number: A30320
 A:Accession: A30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-770 <VIT1>
 A:Accession: B30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 122-288, 'V', 365-770 <VIT2>
 A:Accession: C30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 606-770 <VIT3>
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
 A:Reference number: A31087; MUID:88124954

A:Accession: A31087
 A:Molecule type: mRNA
 A:Residues: 507-770 <ZAI>
 A:Cross-references: GB:M18734; NID:q178572; PIDN:AAA51726.1; PID:q178573
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue 603
 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue 65
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0
 R:Kisters, C.L.; Mulhaup, G.; Stimm, G.; Potlgiesser, J.; Martins, R.N.; Beyreuther, K.

Query Match 100.0%; Score 4058; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 6.5e-210;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MLPELALLLLAAMTARALEVPTDGNAGLLAPQIAMFCGRILMMHMYONGKWDSPSGTK 60
DB 1 MLPELALLLLAAMTARALEVPTDGNAGLLAPQIAMFCGRILMMHMYONGKWDSPSGTK 60
QY 61 TCIDTKEGIILOYCOEYVPELQITNVVEANOPVTIONMCKRCKKCTHPHVIYRCVLG 120
DB 61 TCIDTKEGIILOYCOEYVPELQITNVVEANOPVTIONMCKRCKKCTHPHVIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEDSDVMWGADTDVADGSEDKVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEDSDVMWGADTDVADGSEDKVVEAEVEAEVEE 240
QY 241 EADDEDDEDEDEVEEAEPEEATERTTSIATTTTTSVEVVEAEVVEAEVVEAEVVE 300
DB 241 EADDEDDEDEDEVEEAEPEEATERTTSIATTTTTSVEVVEAEVVEAEVVEAEVVE 300
QY 301 RAMISRWFDVTEGKCAPEFYGGCGGNRNNFTDEYCAVGSAMSQSLKTQOEPLARD 360
DB 301 RAMISRWFDVTEGKCAPEFYGGCGGNRNNFTDEYCAVGSAMSQSLKTQOEPLARD 360
QY 361 PVKLPPTAASPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVMEWEAEERQA 420
DB 361 PVKLPPTAASPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVMEWEAEERQA 420
QY 421 KNLPRADKKAIVIOHFOEVESLEQEAANEROOLVETHNARVEAMLNDRRRLALENYITAL 480
DB 421 KNLPRADKKAIVIOHFOEVESLEQEAANEROOLVETHNARVEAMLNDRRRLALENYITAL 480
QY 481 QAVPRPRHVNMLKKYVRAEQKROHTLKHFEHVRWDPKKAQIRSQVMTHLRIYER 540
DB 481 QAVPRPRHVNMLKKYVRAEQKROHTLKHFEHVRWDPKKAQIRSQVMTHLRIYER 540
QY 541 MNOSLSLLYNPAVAEETQDEVDLLOKEQNSDVLNMTSEPRISYGNALMPSLET 600
DB 541 MNOSLSLLYNPAVAEETQDEVDLLOKEQNSDVLNMTSEPRISYGNALMPSLET 600
QY 601 KTYVELLPVNGEESLDDLOPHWHSFGADSVPAANTENEVEPVARPAADGLTTPRSGSLTN 660
DB 601 KTYVELLPVNGEESLDDLOPHWHSFGADSVPAANTENEVEPVARPAADGLTTPRSGSLTN 660
QY 661 IKTEIEISVKKDAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGGVIAIYVITL 720
DB 661 IKTEIEISVKKDAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGGVIAIYVITL 720
QY 721 VMLKKKQYTSIHGVEVYDAVTPPEERHLSKMOQNGYENPTYKFEFQOMON 770
DB 721 VMLKKKQYTSIHGVEVYDAVTPPEERHLSKMOQNGYENPTYKFEFQOMON 770

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RESULT 2

A49795
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A49795
 R:Podlansky, M.B.; Tolan, D.R.; Selkoe, D.J.

Am. J. Pathol. 138, 1423-1435, 1991
 A:Title: Homology of the amyloid beta protein precursor in monkey and human supports
 A:Reference number: A49795; M01D:91273117
 A:Accession: A49795
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <QD>
 A:Cross-references: GB:M58727; NID:q342062; PIDN:AAA36829.1; PID:q342063
 A:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing

Query Match 88.5%; Score 3590.5; DB 1; Length 695;
 Best Local Similarity 90.1%; Pred. No. 6.2e-185;
 Matches 694; Conservative 1; Mismatches 0; Indels 75; Gaps 1;

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QY 1 MLPELALLLLAAMTARALEVPTDGNAGLLAPQIAMFCGRILMMHMYONGKWDSPSGTK 60
DB 1 MLPELALLLLAAMTARALEVPTDGNAGLLAPQIAMFCGRILMMHMYONGKWDSPSGTK 60
QY 61 TCIDTKEGIILOYCOEYVPELQITNVVEANOPVTIONMCKRCKKCTHPHVIYRCVLG 120
DB 61 TCIDTKEGIILOYCOEYVPELQITNVVEANOPVTIONMCKRCKKCTHPHVIYRCVLG 120
QY 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPGIDKFR 180
DB 121 EFVSDALLVPDKCKFLHOERMDVCETHLHMHTVAKETCSEKSTNLHDYGMLLPGIDKFR 180
QY 181 GVEFVCCPLAESDNVDSADAEDSDVMWGADTDVADGSEDKVVEAEVEAEVEE 240
DB 181 GVEFVCCPLAESDNVDSADAEDSDVMWGADTDVADGSEDKVVEAEVEAEVEE 240
QY 241 EADDEDDEDEDEVEEAEPEEATERTTSIATTTTTSVEVVEAEVVEAEVVEAEVVE 300
DB 241 EADDEDDEDEDEVEEAEPEEATERTTSIATTTTTSVEVVEAEVVEAEVVEAEVVE 300
QY 301 RAMISRWFDVTEGKCAPEFYGGCGGNRNNFTDEYCAVGSAMSQSLKTQOEPLARD 360
DB 301 RAMISRWFDVTEGKCAPEFYGGCGGNRNNFTDEYCAVGSAMSQSLKTQOEPLARD 360
QY 361 PVKLPPTAASPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVMEWEAEERQA 420
DB 361 PVKLPPTAASPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVMEWEAEERQA 420
QY 421 KNLPRADKKAIVIOHFOEVESLEQEAANEROOLVETHNARVEAMLNDRRRLALENYITAL 480
DB 421 KNLPRADKKAIVIOHFOEVESLEQEAANEROOLVETHNARVEAMLNDRRRLALENYITAL 480
QY 481 QAVPRPRHVNMLKKYVRAEQKROHTLKHFEHVRWDPKKAQIRSQVMTHLRIYER 540
DB 481 QAVPRPRHVNMLKKYVRAEQKROHTLKHFEHVRWDPKKAQIRSQVMTHLRIYER 540
QY 541 MNOSLSLLYNPAVAEETQDEVDLLOKEQNSDVLNMTSEPRISYGNALMPSLET 600
DB 541 MNOSLSLLYNPAVAEETQDEVDLLOKEQNSDVLNMTSEPRISYGNALMPSLET 600
QY 601 KTYVELLPVNGEESLDDLOPHWHSFGADSVPAANTENEVEPVARPAADGLTTPRSGSLTN 660
DB 601 KTYVELLPVNGEESLDDLOPHWHSFGADSVPAANTENEVEPVARPAADGLTTPRSGSLTN 660
QY 661 IKTEIEISVKKDAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGGVIAIYVITL 720
DB 661 IKTEIEISVKKDAEFRHDSGYEVHHOKLVFAEDVGSNKGAIIGLMVGGVIAIYVITL 720
QY 721 VMLKKKQYTSIHGVEVYDAVTPPEERHLSKMOQNGYENPTYKFEFQOMON 770
DB 721 VMLKKKQYTSIHGVEVYDAVTPPEERHLSKMOQNGYENPTYKFEFQOMON 770

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RESULT 3

S00350
 Alzheimer's disease amyloid beta protein precursor - rat
 N:Alternate names: beta-A4 amyloid protein
 C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
 C:Accession: S00550; A41245; A39820; S46251
 R:Shivers, B.D.; Hlilich, C.; Malthaupt, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
 EMBO J. 7, 1365-1370, 1988
 A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain
 A:Reference number: S00550; MUID:86312583
 A:Accession: S00550
 A:Molecule type: mRNA
 A:Residues: 1-695 <STR>
 A:Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
 R:Schubert, D.; Schroeder, R.; Lacobdierre, M.; Saitoh, T.; Cole, G.
 Science 241, 223-226, 1988
 A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
 A:Reference number: A41245; MUID:88264430
 A:Accession: A41245
 A:Molecule type: protein
 A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
 A:Note: evidence for heparan sulfate attachment
 R:Hesse, L.; Behr, D.; Masters, C.L.; Malthaupt, G.
 J. Biol. Chem. 266, 8464-8469, 1991
 A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
 A:Reference number: A39820; MUID:91217087
 A:Accession: A39820
 A:Status: Preliminary
 A:Molecule type: protein
 A:Residues: 18-32 <POT>
 A:Experimental source: brain
 C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is of
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase 1
 C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
 F:623-648/Domain: transmembrane #status Predicted <TM>

Query Match 86.1%; Score 3493.5; DB 2; Length 695;
 Best Local Similarity 87.7%; Pred. No. 9.7e-180;
 Matches 675; Conservative 8; Mismatches 12; Indels 75; Gaps 1;

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QY 1 MIPGIALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVONGKWDSPSGTK 60
DB 1 MIPSLALLLLAAMTVRALEVPDGNAGLLAEPOIAMFCGRLNMHMNVONGKWDSPSGTK 60
QY 61 TCIDIRKEGILQCOEYVPELQITNVVEANQPTIQNMCKRGKCKCKTHHPIPRCLVG 120
DB 61 TCIGTREGILQCOEYVPELQITNVVEANQPTIQNMCKRGKCKCKTHHPIPRCLVG 120
QY 121 EFVSADLLVPDKCKFLHQRMDVCEHLHMTVAKETCESEKTNLHDYGMLLPGIDKFR 180
DB 121 EFVSADLLVPDKCKFLHQRMDVCEHLHMTVAKETCESEKTNLHDYGMLLPGIDKFR 180
QY 181 GVEFVCCPLAEESDNDVSDAEEDSDVWVGADTDYADGSEDKYVEVAEEVEEAEEVEE 240
DB 181 GVEFVCCPLAEESDNDVSDAEEDSDVWVGADTDYADGSEDKYVEVAEEVEEAEEVEE 240
QY 241 EADDEDEDEDGGEVEEEAEPEYEATERTSTATTTTTESEVEVEVNCSEQAEKTPC 300
DB 241 EADDEDEDEDGGEVEEEAEPEYEATERTSTATTTTTESEVEEVR----- 288
QY 301 RAMISRWYFDVTEGKCAFFYGGCGGNRNPFTEECMAVCGSAMSOSILKTQEPPLARD 360
DB 289 ----- 288
QY 361 PVKLTPTAATPDVAVDKLTETPGDENENAHFOKAKERLEAKHREMSOVNREMEBAERQA 420
DB 289 ---VPTTAATPDVAVDKLTETPGDENENAHFOKAKERLEAKHREMSOVNREMEBAERQA 345
QY 421 KMLPRADKKAVTQHOEKEVESLEQEAANERQOLVETNARVAMLNDRRRLALENYITAL 480
DB 346 KMLPRADKKAVTQHOEKEVESLEQEAANERQOLVETNARVAMLNDRRRLALENYITAL 405

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QY 481 QAVPRPRHVENMLKKYRAEOKDRQHTLKHFEHYRMVDPKKAQIRSOVMTHLRYIER 540
 DB 481 QAVPRPRHVENMLKKYRAEOKDRQHTLKHFEHYRMVDPKKAQIRSOVMTHLRYIER 540
 QY 481 QAVPRPRHVENMLKKYRAEOKDRQHTLKHFEHYRMVDPKKAQIRSOVMTHLRYIER 540
 DB 481 QAVPRPRHVENMLKKYRAEOKDRQHTLKHFEHYRMVDPKKAQIRSOVMTHLRYIER 540
 QY 541 MNQSLSLLYNPAVAEETQDEVELLOREONYSDDVLANMISSEPRISYGNALMPSLET 600
 DB 541 MNQSLSLLYNPAVAEETQDEVELLOREONYSDDVLANMISSEPRISYGNALMPSLET 600
 QY 601 KTTVELLVNGEFSDDLQPMHSEFADSVSPANTEVEVPVDPARPAADGLTTRPSSGLTN 660
 DB 601 KTTVELLVNGEFSDDLQPMHSEFADSVSPANTEVEVPVDPARPAADGLTTRPSSGLTN 660
 QY 661 IKTEISEVKMDAEFRHDSGVEVHQKLVFPAEDVSNKGAIIIGLVGVIATYIVTL 720
 DB 661 IKTEISEVKMDAEFRHDSGVEVHQKLVFPAEDVSNKGAIIIGLVGVIATYIVTL 720
 QY 721 VMLKKQYTSIHGVEVDAVTPPEERHL SKMQNGYENPTYKPFPEQMON 770
 DB 721 VMLKKQYTSIHGVEVDAVTPPEERHL SKMQNGYENPTYKPFPEQMON 770
 QY 770 VMLKKQYTSIHGVEVDAVTPPEERHL SKMQNGYENPTYKPFPEQMON 770
 DB 770 VMLKKQYTSIHGVEVDAVTPPEERHL SKMQNGYENPTYKPFPEQMON 770

RESULT 4
 A:Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N:Alternate names: proteinase nexin II
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
 C:Accession: A27485; S19727; 149485
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein pr
 A:Reference number: A27485; MUID:861064489
 A:Accession: A27485
 A:Molecule type: mRNA
 A:Residues: 1-695 <YAN>
 A:Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
 A:Experimental source: brain
 R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
 Biochim. Biophys. Acta 1129, 141-143, 1991
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is clos
 A:Reference number: S19727; MUID:92096458
 A:Accession: S19727
 A:Molecule type: mRNA
 A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
 R:Rizumi, R.; Yamada, T.; Yoshikata, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
 Gene 112, 189-195, 1992
 A:Title: Positive and negative regulatory elements for the expression of the Alzheim
 A:Reference number: 149485; MUID:92209998
 A:Accession: 149485
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-19 <RES>
 A:Cross-references: GB:D10603; NID:g220328; PIDN:BA01456.1; PID:g220329
 C:Genetics:
 A:Map position: 16C3
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal kunitz-type proteinase
 C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 85.5%; Score 3468.5; DB 2; Length 695;
 Best Local Similarity 87.3%; Pred. No. 2.1e-178;
 Matches 672; Conservative 6; Mismatches 17; Indels 75; Gaps 1;

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QY 1 MIPGIALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLNMHMNVONGKWDSPSGTK 60
DB 1 MIPSLALLLLAAMTVRALEVPDGNAGLLAEPOIAMFCGRLNMHMNVONGKWDSPSGTK 60
QY 61 TCIDIRKEGILQCOEYVPELQITNVVEANQPTIQNMCKRGKCKCKTHHPIPRCLVG 120
DB 61 TCIGTREGILQCOEYVPELQITNVVEANQPTIQNMCKRGKCKCKTHHPIPRCLVG 120
QY 121 EFVSADLLVPDKCKFLHQRMDVCEHLHMTVAKETCESEKTNLHDYGMLLPGIDKFR 180
DB 121 EFVSADLLVPDKCKFLHQRMDVCEHLHMTVAKETCESEKTNLHDYGMLLPGIDKFR 180

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121 EFVSDALLVPKCKFLHQRNDVCEHLHMTVAKETSEKSTNLHDYGLMLPGCIDKFR 180
181 GVEFVCCPLAESDNDVSADAEEDSDVWVGADTDYADGSEDKVEVAEEVEAEVEE 240
181 GVEFVCCPLAESDNDVSADAEEDSDVWVGADTDYADGSEDKVEVAEEVEAEVEE 240
241 EADDEDEDDEDEVEEAEPEEATERTTSTATTTTTSVEEVEV----- 288
241 EADDEDEDDEDEVEEAEPEEATERTTSTATTTTTSVEEVEV----- 288
301 RAMISRMVETEGCAFFYGGCGGNNDTEVEYCAVGSAMSQSLKTTOEPLARD 360
289 ----- 288
361 PVKLTPTASTPDADVCKLLETTPGDENEHAFQAKERLEAKHREMSQVMEAEERQA 420
289 ---VPTTASTPDADVCKLLETTPGDENEHAFQAKERLEAKHREMSQVMEAEERQA 345
421 KNLPRADKAVIOHFOEKVESLEQEAANEROQLVETHMAREAMLNDRRRLDLENYIAL 405
346 KNLPRADKAVIOHFOEKVESLEQEAANEROQLVETHMAREAMLNDRRRLDLENYIAL 405
481 QAVPRPRHVENMLKKYVAROKROHTLKHFEHVRMVDPKKAQIRSOVMTHLVIER 540
406 QAVPRPRHVENMLKKYVAROKROHTLKHFEHVRMVDPKKAQIRSOVMTHLVIER 465
541 MNOSLSLLYNPAVAEEIODEVDLLOKEONYSDVLANMISEPRISYGNALMPSLET 600
466 MNOSLSLLYNPAVAEEIODEVDLLOKEONYSDVLANMISEPRISYGNALMPSLET 525
601 KTYVELLVNGEESLDDIQQPHSGADSVPAANTEVEPVADARPAADGLTTRPGSLTN 660
526 KTYVELLVNGEESLDDIQQPHSGADSVPAANTEVEPVADARPAADGLTTRPGSLTN 585
661 IKTEIESEVKKDAEFRRHSGVEVHHOKLVFEAEVGSNKGATIGLVGCVIATVITL 720
585 IKTEIESEVKKDAEFRRHSGVEVHHOKLVFEAEVGSNKGATIGLVGCVIATVITL 645
721 VMLKKKQYTSIHGVEVDAVTPERHLKSKQONGENPTYKFEFQOMON 770
646 VMLKKKQYTSIHGVEVDAVTPERHLKSKQONGENPTYKFEFQOMON 695

RESULT 5
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
Species: Xenopus laevis (African clawed frog)
Date: 10-Jun-1993 #sequence #revision 10-Jun-1993 #text-change 13-Aug-1999
Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1566, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OK>
A:Cross-references: GB:S52417; NID:9263150; PIDN:AA824853.1; PID:9263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 83.9%; Score 3403.5; DB 2; Length 747;
Best Local Similarity 85.2%; Pred. No. 7e-175;
Matches 645; Conservative 40; Mismatches 45; Indels 27; Gaps 5;

17 ALEVPDAGGLAEPQIAF-CGRLLNMHNNQNGKMDSPGKTCIDTKRGIIQYOE 75
15 ALEVLVDGGLAEPQIAF-SVARLNMHNNQNGKMDSPGKTCIDTKRGIIQYOE 71
76 VPELQITNVVANOPVTIONMCKGRKCKTHPHFVIRPCLVGEFVSALLVPDKCF 135

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72 VPELQITNVVANOPVTIONMCKGRKCKRTHIVVPCLVGEFVSALLVPDKCF 131
136 LHQRNDVCEHLHMTVAKETSEKSTNLHDYGLMLPGCIDKRGVYCCPLAESDN 195
132 LHQRNDVCEHLHMTVAKETSEKSTNLHDYGLMLPGCIDKRGVYCCPLAESDN 191
196 VDSADAEEDSDVWVGADTDYADGSEDKVEVA--EEVEAEVEEADDEDEDDE 253
192 FDSADAEEDSDVWVGADTDYADGSEDKVEVA--EEVEAEVEEADDEDEDDE--DCDE 249
254 VEEAEPEEPEEATERTTSTATTTTTSVEEVEVREVCSEQAEOPCRAMISRMVET 313
250 AEEPEPEEPEEATERTTSTATTTTTSVEEVEVREVCSEQAEOPCRAMISRMVET 309
314 GKCAFFYGGCGGNNDTEVEYCAVGSAMSQSLKTTOEPLARDPVKLTPTASTPD 373
310 SKCAFFYGGCGGNNDTEVEYCAVGSAMSQSLKTTOEPLARDPVKLTPTASTPD 350
374 AVDKYLETTPGDENEHAFQAKERLEAKHREMSQVMEAEERQA 433
351 AVDKYLETTPGDENEHAFQAKERLEAKHREMSQVMEAEERQA 410
434 HFOEKVESLEQEAANEROQLVETHMAREAMLNDRRRLDLENYIALQAVPRPRHVEN 493
411 HFOEKVESLEQEAANEROQLVETHMAREAMLNDRRRLDLENYIALQAVPRPRHVEN 470
494 LKKYVAROKROHTLKHFEHVRMVDPKKAQIRSOVMTHLVIERMNOSLSLLYNPA 553
471 LKKYVAROKROHTLKHFEHVRMVDPKKAQIRSOVMTHLVIERMNOSLSLLYNPA 530
554 VAEETIODEVDLLOKEONYSDVLANMISEPRISYGNALMPSLETKTYVELLVNGEE 613
531 VAEETIODEVDLLOKEONYSDVLANMISEPRISYGNALMPSLETKTYVELLVNGEE 590
614 SLDDIQQPHSGADSVPAANTEVEPVADARPAADGLTTRPGSLTNIKTEIESEVKKDA 673
591 NIEDIQQPHSGADSVPAANTEVEPVADARPAADGLTTRPGSLTNIKTEIESEVKKDA 650
674 EFRHDSGYEVHHOKLVFEAEVGSNKGATIGLVGCVIATVITLVMKKKQYTSIH 733
651 EFRHDSGYEVHHOKLVFEAEVGSNKGATIGLVGCVIATVITLVMKKKQYTSIH 710
734 GVEVDAVTPERHLKSKQONGENPTYKFEFQOMON 770
711 GVEVDAVTPERHLKSKQONGENPTYKFEFQOMON 747

RESULT 6
A32761
hypothetical Alzheimer's disease amyloid beta protein, Alu-containing clone - human
Species: Homo sapiens (man)
C:Date: 29-Jan-1990 #sequence #revision 10-Apr-1996 #text-change 10-Apr-1996
C:Accession: A32761
R:de Sauvage, F.; Octave, J.N.
Science 245, 651-653, 1989
A:Title: A novel mRNA of the A4 amyloid precursor gene coding for a possibly secreted
A:Reference number: A32761; MUID:89346754
A:Accession: A32761
A:Molecule type: mRNA
A:Residues: 1-484 <DES>
A:Cross-references: GB:M28373
A:Note: the authors translated the codon ATG for residue 433 as Ieu
C:Comment: This is the hypothetical translation of a sequence believed to contain cl
C:Keywords: cloning artifact

Query Match 60.3%; Score 2446.5; DB 4; Length 484;
Best Local Similarity 95.9%; Pred. No. 7.3e-124;
Matches 463; Conservative 1; Mismatches 0; Indels 19; Gaps 1;

80 LQITNVVANOPVTIONMCKGRKCKTHPHFVIRPCLVGEFVSALLVPDKCF 139
1 LQITNVVANOPVTIONMCKGRKCKTHPHFVIRPCLVGEFVSALLVPDKCF 60

```

QY 140 RMDVCEHLHMTVAKETSEKSTNLHDYGMLLPCGIDKFRGVEVCCPLAEESDNDVSA 199
 |||||||
 Db 61 RMDVCEHLHMTVAKETSEKSTNLHDYGMLLPCGIDKFRGVEVCCPLAEESDNDVSA 120
 |||||||
 QY 200 DAEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEEEDDEDEDGDEVEEAE 259
 |||||||
 Db 121 DAEDSDVWVGADTDYADGSEDKVVEVAEEVEAEVEEEDDEDEDGDEVEEAE 180
 |||||||
 QY 260 EYEEETETSTTATTTTTTSTVEEVVREVCSEQAETGPCRAMISRWFEDTEGCAFP 319
 |||||||
 Db 181 EYEEETETSTTATTTTTTSTVEEVVREVCSEQAETGPCRAMISRWFEDTEGCAFP 240
 |||||||
 QY 320 FYGGCGGNRRNFDTEEYCAVCSAMSOSLTKTOPLARDPVKLTPTTASTDPAVDKYL 379
 |||||||
 Db 241 FYGGCGGNRRNFDTEEYCAVCSA-----ITTTASTPDAVDKYL 281
 |||||||
 QY 380 EYPGDENHAFHOKAKERLEAKHREMSQVMREWEAEQAQNLPRADKAVIQHFOEKY 439
 |||||||
 Db 282 EYPGDENHAFHOKAKERLEAKHREMSQVMREWEAEQAQNLPRADKAVIQHFOEKY 341
 |||||||
 QY 440 ESLDEEAAREQOIVETHNARVEMINDRRRLALENYITALQAVPPRRHVFNMKKYR 499
 |||||||
 Db 342 ESLDEEAAREQOIVETHNARVEMINDRRRLALENYITALQAVPPRRHVFNMKKYR 401
 |||||||
 QY 500 ABOKDRHHTLKHFEHVRMVPKKAQIRSOVMTLHVIERMNSLSLYNPVAAVEIO 559
 |||||||
 Db 402 ABOKDRHHTLKHFEHVRMVPKKAQIRSOVMTLHVIERMNSLSLYNPVAAVEIO 461
 |||||||
 QY 560 DEV 562
 ||||
 Db 462 DEV 464

RESULT 7

A49321
 Amyloid beta (A4) homolog 2 precursor - human
 N:Alternate names: CDEI-binding protein
 C:Species: Homo sapiens (man)
 C>Date: 24-Feb-1994 #sequence-revision 18-Nov-1994 #text-change 13-Aug-1999
 C:Accession: A49321; S34644; S40519
 R:Spencer, C.A.; Grant, F.J.; Grimm, G.; O'Hara, P.J.; Norris, F.; Norris, K.; Foster, Biochemistry 32, 4481-4486, 1993
 A>Title: Molecular cloning of the cDNA for a human amyloid precursor protein homolog: ev
 A:Reference number: A49321; MUID:93250009
 A:Accession: A49321
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-763 <SPR>
 C:Cross-references: GB:S60099; NID:G300168; PIDN:MAC60589.1; PID:G300169
 Experimental source: Placenta
 A>Note: sequence extracted from NCBI backbone (NCBIN:131198, NCBI:P131199)
 R:yon der Kammer, H.; Klaudiny, J.; Hanes, J.; Schell, K.H.
 submitted to the EMBL Data Library, April 1993
 A:Description: The human homologue of the murine CDEI binding protein is an amyloid pred
 A:Reference number: S34644
 A:Accession: S34644
 A:Molecule type: mRNA
 A:Residues: 1-763 <YON>
 A:Cross-references: EMBL:Z22572; NID:G394763; PIDN:CAA80295.1; PID:G394764
 R:Masco, W.; Gurubhagavata, S.; Paradis, M.; Romano, D.M.; Sisodia, S.S.; Hyman, B.T.; Nature Genet. 5, 95-99, 1993
 A>Title: Isolation and characterization of APLP2 encoding a homologue of the Alzheimer's
 A:Reference number: S40519; MUID:94035131
 A:Accession: S40519
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-763 <MAS>
 C:Cross-references: GB:L27631; NID:G450391; PIDN:AAC41701.1; PID:G450392
 C:Genetics:
 A:Gene: GDB:APLP2; APLP2
 A:Cross-references: GDB:139159; OMIM:104776
 A:Map position: 11q23-11q25

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteins
 C:Keywords: alternative splicing; transmembrane protein
 F:310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPT>

Query Match 48.8%; Score 1981.5; DB 2; Length 763;
 Best Local Similarity 50.4%; Pred. No. 1e-98;
 Matches 408; Conservative 127; Mismatches 166; Indels 107; Gaps 21.

QY 5 LALLLAAVTARALEV-----PTDGNAG--LLAEQIAMFCGRIMNHNVONGKWDSDP 56
 |||||
 Db 15 LLLLLVLTALALAGYIEALANAGFAVAEPQIAMFCGRIMNHNVIOGTQKWEPP 74
 |||||
 QY 57 SGTTCIDTKKEILLQCEVPELQITNVVNEQVTONCKRKRCKOCTPHRVIPR 116
 |||||
 Db 75 TGTKSCFETKEEVLOYCEMPELQITNVVNEQVTONCKRKRCKOCTPHRVIPR 132
 |||||
 QY 117 CLVGFVSDALVDPKCFELHQRMDVCEHLHMTVAKETSEKSTNLHDYGMLLPCGI 176
 |||||
 Db 133 CLVGFVSDVLLVPEKCGFHKERMDEVCENQHMTTVKCACTLQGMILYSGMILLPCGV 192
 |||||
 QY 177 DKFRVEVCCPLAEESDNDVSADEEDSDVWVGADTDYADGSEDKVVEVAEEVEAE 236
 |||||
 Db 193 DQFHGTVEVCCPQTKIISVSKEEEDDE-----EEDEDEDEDDYVKKSEFPTEAD 245
 |||||
 QY 237 VEE--EAA--DDEDEDGDEVEEAE-----EYEEAERTSTATTTTTTSTVE 284
 |||||
 Db 246 LEDFTEAIVDEDEDDEEVEEVEDRDYVDTFKGDDTNE--ENPTGSDGTMKDETT 303
 |||||
 QY 285 EYVREVCSEQAETGPCRAMISRWFEDTEGCAFPFYGGCGGNRRNFDTEEYCAVCSA 344
 |||||
 Db 304 HDVKAVCQEAATGCPRAVMPRWFDLSKGCVRITYGCGGNRRNFDSEDCMAVCSAM 363
 |||||
 QY 345 MSQSLKTTQEPPLARDPVKLTPTTASTDPAVDKYLETGEDENHAFHOKAKERLEAKHRE 404
 |||||
 Db 364 I-----PPPLPT-----NDVVPETPSADNEHARFQAKOLEIRHN 403
 |||||
 QY 405 RMSQVMREWEAEQAQNLPRADKAVIQHFOEKVESLEQEAAREQOIVETHNARVEM 464
 |||||
 Db 404 RMDRKKHEBERELQAKMLPRAEROTLIHQAMKALEKASKQOIVETHNARVEM 463
 |||||
 QY 465 LNDRRRLALENYITALQAVPPRRHVFNMKKYRABQKDRHHTLKHFEHVRMVPKKA 524
 |||||
 Db 464 LNDRRRLALENYITALQSDPPRRHIIQALRRYVAEKDRHHTIRHVOHVLAVDPEKAA 523
 |||||
 QY 525 QIRSOVMTLHVIERMNSLSLYNPVAAVEIODEVELLOKQONSDVILAMISBP 584
 |||||
 Db 524 QIRSOVMTLHVIERMNSLSLYKPYVAOIEIDELQEQOR-----ADM--- 572
 |||||
 QY 585 RISYGNALMPSLFTTKTVVELLPVNGEFLDDLOPMHSPGADSVAPANTENEVEVDAR 644
 |||||
 Db 573 -----DQFTASISETPVDR---VSSEES--EELPPHPF--HPPALPENE---DTP 616
 |||||
 QY 645 AADRGLTPRGSGLTN-----IKTEE--ISEVKDAEFRRDGSYEVHOKLVFAEDVG 696
 |||||
 Db 617 ELYHNM--KKSGVGEOGGLIGAEKVINSKNKVDENMVIDETLDV--KEIIFAEVNG 672
 |||||
 QY 697 S-----NKAIIIGLVAGGVATVITVLMKKKQYTSIHGCVED 739
 |||||
 Db 673 GLEEBRESVGLREDESLSSALIGLIVAVATVIVISLVMLKKROYGTISHGIVEVD 732
 |||||
 QY 740 AAVTPPEERHLSKMOONGENPTVYKFEQMO 769
 |||||
 Db 733 PMLPPEERHLSKMOONGENPTVYKFEQMO 762
 |||||

RESULT 8

S42880
 amyloid precursor-like protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 06-Jan-1995 #sequence-revision 06-Jan-1995 #text-change 17-Mar-1999
 C:Accession: S42880; S47528
 R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
 submitted to the EMBL Data Library, March 1994

A:Description: Complete nucleotide ad deduced amino acid sequence of rat amyloid precursor
 A:Reference number: S42880
 A:Accession: S42880
 A:Molecule type: mRNA
 A:Residues: 1-765 <SANT>
 A:Cross-references: EMBL:X77934
 R:Sandbrink, R.; Masters, C.L.; Beyreuther, K.
 Biochim. Biophys. Acta 1219, 167-170, 1994
 A:Title: Complete nucleotide and deduced amino acid sequence of rat amyloid protein precursor
 A:Reference number: S47528; MUID:94368849
 A:Accession: S47528
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-765 <SA2>
 A:Cross-references: EMBL:X77934
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing
 F:312-362/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 48.6%; Score 1971.5; DB 2; Length 765;
 Best Local Similarity 49.7%; Pred. No. 3.6e-98;
 Matches 401; Conservative 134; Mismatches 173; Indels 99; Gaps 20;

```

QY 5 LALLLLAAMTAALEV-----PTGDNAG---LLAEPOIAMFCGRIMHMHNVONGKWDSDP 56
DB 15 LVLVLLGLTPAAPAALAGITALEALANAGTGRAVAEPQIAMFCGLMHHVNIOTGKWEHPD 74
QY 57 SGTKCIDTKEGILQYCOEYVPPELOITNVNEANQVPTIONMCKRGKCKTTPHPIVPIYR 116
DB 75 TGTKSCICTKEVLYQCOEYPELOITNVMEANQVNIIDSMCRDRCKCRS--HIVIFPK 132
QY 117 CLVGEFVSVDALLVPDKCKFLHOERNDVCETHLHMTTVAKECTSEKSTNLHDYGMLLPGCI 176
DB 133 CLVGEFVSVDLVLPNCOEYFHOERMEVCEKHQRMHTLVKCACTGLTGLYSGLMLPGCV 192
QY 177 DKFRGEFVFCPLAE--ESDNVDSADAEEDSDVMWGAADTYA--DGSDEKVEVEAEE 233
DB 193 DOFHGTEYVCCPQTYKTVSDSTMSKEEEEEE---DEEEDYALDKSEFPFEADLEDT 248
QY 234 VAEEVEEADDEDEDEDEVEEAEPEYEE-----ATERTTSIATTTTTTSEVEEV 287
DB 249 EAAADEDEDEDEDEDEGEVEVEDRDYYDFSGDDYDNEINTEPSSDQTSIDKEIAHDV 308
QY 288 REVCSQAEQETGPRAMISRWYFDVTEGKCAPFFYGGCGGGRNNFTDEYCAVVCSSASQ 347
DB 309 KAVCSQEAETGPRAMVPMWYFDLSKGCVRPIYGGCGGRNNFSESDYCAVVCSTMI-- 366
QY 348 SLKTTQETPLARDPVKLPPTASTPDVADKYLETGPDENEHAPQAKERLAKRERMS 407
DB 367 -----PPTPLPT-----NDVDYFETSDADNEHARFQAKERQLEIRHRSMD 408
QY 408 QVAREMEAEARQAKNLPKADKRAVIOHFOEKVESLEQEAANERQOLVETHMARVEAMLD 467
DB 409 RVKKEEAEELQAKNLPKAREQTLIOHFOAMVKALEKSAESKQOLVETHLARVEAMLD 468
QY 468 RRLALENTITLQAVPPRPRAVFMKLKYYAAEQDKORHTLKHFEHVAMPVPRKAAQDR 527
DB 469 RRLALENTITLQAVPPRPRAVFMKLKYYAAEQDKORHTLKHFEHVAMPVPRKAAQDR 528
QY 528 SGMVHLRYIYERMNOSLILYNPAVAEIODEVDELLOKCONSDVLANMISPRIS 587
DB 529 SGMVHLRYIYERMNOSLILYNPAVAEIODEVDELLOKCONSDVLANMISPRIS 587
QY 588 YGNDALMPSLETETKTVELLPVNGEFSLDLQPMHSGADSVANTENEVEPVADAPAD 647
DB 575 ---DOFTSISENPVDVR---VSSEES--EIPPFHLPF--HPPSLSENE---DTPPELY 621
QY 648 RGLTTRPGSGCLTN-----IKTEE---ISVYKMADEFRHDSGEVYHOKKVFPAEDVGS-- 697
DB 622 HPM--KKGSGMAEQDGLGAEKVIYNSKNKMDENNYIDETLDV--KENIINAERVGGLE 677
QY 698 -----NKGAIIGLWGVVIATVIVITVLMKKKQYTSIHGVEVDAV 742
DB 698 -----NKGAIIGLWGVVIATVIVITVLMKKKQYTSIHGVEVDAV 742

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DB 678 EEPDSVGLREDFSLSSALGLLVIAVAITVIVISLWMLRKROYGTHSHGIVEVHPML 737
 QY 743 TPERRHLSKMQONGENTTYFFEQMQ 769
 DB 738 TPERRHLSKMQONGENTTYFFEQMQ 764

RESULT 9

A49974
 beta-amyloid precursor protein 2 homolog APLP2 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
 C:Accession: A49974
 R:Stuntz, H.H.; Thinakaran, G.; Von Koch, C.; Lo, A.C.; Tanzi, R.E.; Sisodia, S.S.
 J. Biol. Chem. 269, 2637-2644, 1994
 A:Title: Expression of a ubiquitous, cross-reactive homologue of the mouse beta-amyloid
 A:Reference number: A49974; MUID:94132029
 A:Accession: A49974
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-751 <SLU>
 A:Cross-references: GB:U1571; NID:9558467; PIDN:AAA50603.1; PID:9558468
 A>Note: sequence extracted from NCBI backbone (NCBI:144636)
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 F:310-360/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 48.2%; Score 1956.5; DB 2; Length 751;
 Best Local Similarity 49.3%; Pred. No. 2.2e-97;
 Matches 397; Conservative 130; Mismatches 169; Indels 109; Gaps 20;

```

QY 5 LALLLLAAMTAALEV-----PTGDNAG---LLAEPOIAMFCGRIMHMHNVONGKWDSDP 56
DB 15 LVLVLLGLTPAAPAALAGITALEALANAGTGRAVAEPQIAMFCGLMHHVNIOTGKWEHPD 74
QY 57 SGTKCIDTKEGILQYCOEYVPPELOITNVNEANQVPTIONMCKRGKCKTTPHPIVPIYR 116
DB 75 TGTKSCICTKEVLYQCOEYPELOITNVMEANQVNIIDSMCRDRCKCRS--HIVIFPK 132
QY 117 CLVGEFVSVDALLVPDKCKFLHOERNDVCETHLHMTTVAKECTSEKSTNLHDYGMLLPGCI 176
DB 133 CLVGEFVSVDLVLPNCOEYFHOERMEVCEKHQRMHTLVKCACTGLTGLYSGLMLPGCV 192
QY 177 DKFRGEFVFCPLAE--ESDNVDSADAEEDSDVMWGAADTYADGSEKVEVEAEE-- 231
DB 193 DOFHGTEYVCCPQTYKTVSDSTMSKEEEEEE-----DEEEDYALDKSEFPFE 243
QY 232 BEVAEEVEEAD--DEDEDEDEGEVEEAE-----EPYEATERTTSIATTTTTTSES 282
DB 244 ADLEDFTEAANDDEEEDDEGEVEVEDRDYYDFPKGDYNE--ENPEPSSGEGTISQKE 301
QY 283 VEEVREVCSQAEQETGPRAMISRWYFDVTEGKCAPFFYGGCGGGRNNFTDEYCAVVCSS 342
DB 302 IVHDVKAVCSQEAETGPRAMVPMWYFDLSKGCVRPIYGGCGGGRNNFSESDYCAVVC 361
QY 343 SAMSQSLKTTQETPLARDPVKLPPTASTPDVADKYLETGPDENEHAPQAKERLAKRERMS 402
DB 362 AMT-----PPTPLPT-----NDVDYFETSDADNEHARFQAKERQLEIRH 401
QY 403 ERMQVAREMEAEARQAKNLPKADKRAVIOHFOEKVESLEQEAANERQOLVETHMARVE 462
DB 402 RRMQVAREMEAEARQAKNLPKAREQTLIOHFOAMVKALEKSAESKQOLVETHLARVE 461
QY 463 AMLNDRRLALENTITLQAVPPRPRAVFMKLKYYAAEQDKORHTLKHFEHVAMPVPRK 522
DB 462 AMLNDRRLALENTITLQAVPPRPRAVFMKLKYYAAEQDKORHTLKHFEHVAMPVPRK 521
QY 523 AAQISQVMTHLRYIYERMNOSLILYNPAVAEIODEVDELLOKCONSDVLANMIS 582
DB 522 AAQISQVMTHLRYIYERMNOSLILYNPAVAEIODEVDELLOKCONSDVLANMIS 572
QY 583 EPRISYGDALMPSLETETKTVELLPVNGEFSLDLQPMHSGADSVANTENEVEPVDA 642
DB 573 -----DOFTSISENPVDVRVSSESE--EIPPFHLPF-----PSISENE----- 612

```

QY 643 RPAADRGTLTPRSGSLTNKTEEI-SEVKMADEFRHDSGYEVHOKLVFAEDVGS---- 697
 DB 613 -----GSGMAEQDG-GLIGAEKVIYNSKMKMDENWIDELTDV--KEMTNAERVGLEEE 665
 QY 698 -----NKGAILGMVGVVATVIVITLMLKKROYTSIHGVEVDAAVTP 744
 DB 666 PESVGRFLREDFSSNALIGLLVIAVAITVIVISLVMLRKROYGTSIGIYEVDPMLTP 725
 QY 745 EERRLSKMQONGENPTYKFFEQMQ 769
 DB 726 EERRHLMKQNGENPTYKYLEOMQ 750

RESULT 10
 A46362
 amyloid precursor-like protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
 Accession: A46362
 Acc. Natl. Acad. Sci. U.S.A. 89, 10758-10762, 1992
 A:Title: Identification of a mouse brain cDNA that encodes a protein related to the Alzheimer's disease amyloid beta protein; animal Kunlitz-type proteinase 1
 A:Reference number: A46362; MUID:93066322
 A:Accession: A46362
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-653 <MAS>
 A:Experimental source: brain
 A:Note: sequence inconsistent with the nucleotide translation
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunlitz-type proteinase 1
 C:Keywords: transmembrane protein

Query Match 28.4%; Score 1150.5; DB 2; Length 653;
 Best Local Similarity 35.4%; Pred. No. 2.7e-54;
 Matches 274; Conservative 120; Mismatches 228; Indels 153; Gaps 19;

QY 1 MLPGLALLLAWMTARA-LEVPPTDGNAGLLAPOTIAMCGRLMMHNNONGKWDSPSGT 59
 DB 22 LLP-LSLILRLQALVGNLAVGSPSAEAPGSAQVAGLCGLITLRLDLRTGKMEPDPORS 80
 QY 60 KTCIDTKEGILQCYGEVYPELQITVNEANQPTIQNMCKRGRKCKTHPHF-VIYRCL 118
 DB 81 RRCILDPRQVLEYCRQMPDELHIAVEQAQAIPIERMCGGTRSCARPHHEVYVPFCL 140
 QY 119 VGEFSDALIVPDKKFLHQRMDVCEFHILHHTYAKETCSKSTNLNDYGLMLCGIDK 178
 DB 141 PGEFVSEALIVPEGRFLEHQRMDCESTRRHOAEACSSQGLILHSGMLLPCGSDR 200
 QY 179 FGVGEVCCPLAEESDNDVSDAEEDSDVW-WGAGADTDYADGSDKVEVAEEVAV 237
 DB 201 FRGVYVCCP-PRATPNRSGMAAGDPSTRSMPLGR---AAGGD-----EEVESF 248
 QY 238 EEEEDDEDEDDEGEVEEAEPEYEATERTTSIATTTTTTSEVVEVVCSEQAE 297
 DB 249 POPVDYVEVPEQAEVEEERAPPPSSHP----- 281
 QY 298 GPCRAMIRMYFVEGKCAPFFYGCGGNRNPTTEECMAVCGSAMSQSLKTTQEP 357
 DB 282 -----VWVS-----VT----- 288
 QY 358 ARDPKLTPTTASTPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVMREME 417
 DB 289 ---PFRPT-----DGVDFYFGMGEIGEHGFLRAKMDLEERMRQINEMRMAAD 339
 QY 418 RQAKMLPRADKKAIVQHFQEKVESLEQEAANEQOLVETHHARVAMLNDRRRLALENY 477
 DB 340 SOSKMLPRADROLNEHFQSIQTLQLEQVSGERQVLETHATRVATALLNDORRALTEFL 399
 QY 478 TALQAVPRPRHVENMLKKYVABOKDQROHTLKHFEHRMVDPKKAADIRSQVTHLAV 537
 DB 400 AALQDPPQAEERVLMALRKYLEKQEQRHLLRHQVAAVDEPKAQQMRFOVTHLQVI 459

QY 538 VERMNSLSLYNPAVAEITODEVELLOKRONYSDDVLANMISEPRISYGNALMP-S 596
 DB 460 EERMNSIGLDQNPRLQOELRPQIOELL-----LASHLPSEL---DASVPS 505
 QY 597 LRETFTVELLPVNGEFLDQPMHSGADSPANTENEVEPVVAPRADGLTTPRGS 656
 DB 506 SSEDK-----GSLQ-----PESKDRPYTLF---KGSIDQESS 536
 QY 657 GLTNIKTEISEVKMADEFRHDSGYEVH--QKLVFAEDVGSNKGAILGLMVGYYIA 713
 DB 537 SSGREKLTPLEQYEQKVNASAPRGPFHSDIQDELAPSGVGERALSGILLMGAGG 596
 QY 714 TVIVITVYML-KKROYTSIHGVEVDAAVPEERHLSKMQONGENPTYKFFEQ 767
 DB 597 SLIVSLTLRLKKRPYGTISHGVEVDPMLTEEQOLRELQHHGVEENPTYRLEE 651

RESULT 11
 JCI1404
 CDEI-box DNA-binding protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
 Accession: JCI1404
 R:Vidal, F.; Bianzy, A.; Rassoulzadegan, M.; Guzin, F.
 Biochem. Biophys. Res. Commun. 189, 1336-1341, 1992
 A:Title: A murine sequence-specific DNA binding protein shows extensive local similarity
 A:Reference number: JCI1404; MUID:93129193
 A:Accession: JCI1404
 A:Molecule type: mRNA
 A:Residues: 1-511 <VID>
 C:Comment: This protein plays an important role in the early development of the mouse
 C:Keywords: DNA binding; transmembrane protein

Query Match 27.4%; Score 1112.5; DB 2; Length 511;
 Best Local Similarity 43.0%; Pred. No. 2.2e-52;
 Matches 264; Conservative 87; Mismatches 136; Indels 127; Gaps 21;

QY 174 CGIDFRVEVCCPLAEESDNDVSDAEEDSDVWVGADTDYADGSEDKVEVAEE 233
 DB 6 CGVDQFQTEYVCCP---QRTVDS-----DSTMK----- 37
 QY 234 VAEVEEADDEDDEDDEDEVEEAEPEYEATERTTSIATTTTTTSEVVEVVCSE 293
 DB 38 ---EEDEDEDEDEYDLKSEFPTEADLDEPTE---AADEEEDDEGEVYVD----- 86
 QY 294 QAEFGPCRAMISRMYEDVTEGKCAPFFYGCGGNRNPTTEECMAVCGSAMSQSLKTT 353
 DB 87 -----RDYYD-----PF-----KGDYENENPTE-----PSSEGTI--S 114
 QY 354 QEPLARDVYKLTPTAASPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVMRE 413
 DB 115 DKEIYHD-VKYPPTPLPTND-VDYFETSDADNEARQKAKBOLEIHRNRMDVYKRW 172
 QY 414 EEAERQANLPRADKKAIVQHFQEKVESLEQEAANEQOLVETHHARVAMLNDRRRLAL 473
 DB 173 EEAELQANLPRADKKAIVQHFQEKVESLEQEAANEQOLVETHHARVAMLNDRRRLAL 232
 QY 474 ENYITLQAVPRPRHVENMLKKYVABOKDQROHTLKHFEHRMVDPKKAADIRSQVTH 533
 DB 233 ENYLAALQSDPPRPRHRIQALRRYVRAENKDRILTHRYQVLAVDPEKAAQMSQVTH 292
 QY 534 LRAVYERNOSLSLYNPAVAEITODEVELLOKRONYSDDVLANMISEPRISYGNAL 593
 DB 293 LRAVYERNOSLSLYKVPYAEQTEIDELQDQ-----ADM-----DQF 335
 QY 594 MSLTEFTYVELLPVNGEFLDQPMHSGADSPANTENEVEPVVAPRADGLTTPRGS 653
 DB 336 TSSISENPDVRYVSESE-ETPPPHPLHF-----PSLSNE-----GSGMAEQ 379
 QY 654 PGSLTNKTEEI-SEVKMADEFRHDSGYEVHOKLVFAEDVGS----- 697
 DB 380 DG-GLIGAEKVIYNSKMKMDENWIDELTDV--KEMIFNAERVGLEEPESVGRFLREDF 436

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OY 698 --NKAIIIGMVGWVIAITVITLMLKKQYTSIHNGVGVDAAVPREEHNSKMOON 755
Db 437 SLSNALIGLIVAIYVIVISLVMRLKROYGTISHGIVEVDMLPREEHNLKMOH 496
OY 756 GYENPTYKFEQOMQ 769
Db 497 GYENPTYKFEQOMQ 510

RESULT 12
T15795
hypothetical protein C42D8.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000
C:Accession: T15795; A49414
R:Hallsworth, K.
submitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans cosmid C42D8.
A:Reference number: Z18405
A:Accession: T15795
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-686 <HA>
A:Cross-references: EMBL:U56966; NID:g1293844; PID:g1293850; PIDN:AAA98722.1; GSPDB:GN00
A:Experimental source: strain Bristol N2; clone C42D8
R:Daigle, I.; Li, C.
Proc. Natl. Acad. Sci. U.S.A. 90, 12045-12049, 1993
A:Title: ap1-1, a Caenorhabditis elegans gene encoding a protein related to the human be
A:Reference number: A49414; MUID:94089766
A:Accession: A49414
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 7-686 <DAI>
A:Cross-references: GB:U00240; NID:g416296; PIDN:AAC46470.1; PID:g416297
C:Genetics:
A:Gene: CESP:C42D8.8
A:Map position: X
A:Introns: 22/3: 78/3; 121/1; 199/1; 230/1; 274/3; 344/3; 410/2; 471/2; 537/3; 580/3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

Query Match 19.3%; Score 785; DB 2; Length 686;
Best Local Similarity 26.8%; Pred. NO. 1.1e-34;
Matches 224; Conservative 111; Mismatches 272; Indels 230; Gaps 23;

OY 1 MLPGALILLAAWTRALEVPTDGNAGLLAEPOIAFCGRLLMMHNVQNGKWDSPSGTK 60
Db 6 IMIGLILPIIVA-TYYAEGSPAGSKRHEKFTIPVAFSCGYRQYM-TEGSKTKTDERA 63
OY 61 TCIDTRREGILOYCOEYVPELOITNVVEANQPYTIONMCKRGKROCKTHPEVYIPRCLVG 120
Db 64 TCFSGKLIDILKCRKRAYPAMNITNIVEYSHEVISIDMCEEESPK-WTHSVRPYHCIDG 122
OY 121 EYVSADLVLPDKCKFLHQERMDVCETHLHMHTVAKETGSEKSTN-----LHDYGMLLPC 174
Db 123 EHSSESLQVPHDCQSHVNSRDQNDYQHKMDAGKQCKTKSKGNKMDITVSFVLEPC 182
OY 175 GIDKRGVEYVCCPLAESDNDVSDAEBEDSDVVMWGADTDYADGSEDKVVEVAEEBV 234
Db 183 ALDMFGEYFVCCP-----NDQTKTIDVQTK----- 209
OY 235 AEVEEAEADDDDDDEGDGDEVEEAEPEYEATERTTSIATTTTTTESEVEYVREVCBQ 294
Db 210 ---EDDDDDDEDADVEDDYSESDKDEE----- 236
OY 295 AETGPCRAMISRMYEDVTGKCAPEFYGGCGGNRNRFTEYCMAVCGSAMSOILKTTQ 354
Db 237 ----- 236
OY 355 EPLARPPVLLPTTAASPDAVDKYLETPGDDENDHAFQAKRLEAKHERRSYQWREWE 414
Db 237 EESSDDP-----YKRIANWTNEHDFCAKRMDEKAKKIDKDYKWKENG 280

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QY 238 EE-EAADDDEDDDEVEEAEEPEYEA-TERTSIATTTTTTTSVEEVREVCSEQA 295
 DB 297 DSGEDNDNEEDGAGSESEAEVEASWDGSGAKVYSLKSDSSPSAPAPAPAPAPYKS 356
 QY 296 EFGPCRAMISRMVFDYTESKAPFFYGGCGGNRNNDTEEYCMAGSAMOSLKTTOE 355
 DB 357 ESVTSTPOLST-----ASAFAAFAANSNGSGT-----GAGAPSTQAQPSD 396
 QY 356 PLARPPVKLTPTAASPDVNDKYLETFGDENEHAFQAKERLEAKHRMRMGOVRENEE 415
 DB 397 P-----YFTHFDPHYEHOSYKVSQKRLSHREKVTIRVAKDMSD 435
 QY 416 AERQAKNLPKADKA-----VIOFQKVESELEQEAANEQOLVETMAVEAMLNDR 468
 DB 436 LEEKYQDMMLADPKAAOSKQKMTARFQTSVQALEEENAEKHQOLAAHQOVLAHINR 495
 QY 469 RRLAENITTAQAVPPRPRHVENMKKYVRAEQKROHTLKHFEH-VKMDP---KKA 524
 DB 496 KREAMTCYQALTEQPPNANHKEKLOKLLRALHRAHALAHYHLLNSGGPGLTMAA 555
 QY 525 QIRSOVMTHLRYIERMNOSISLTVNPAVAEI-----QDEV----- 562
 DB 556 SERPTLERLIDRAVNSMTMLKRYLPESLAKIAQLMNDYTLARSKDIDPSSIGMSE 615
 QY 563 -----DELQKQNYSDOVLAN 579
 DB 616 EAEAGILDKRYEIRKVAEKERLAEKQKQRAEREKREKRLREAKKVDMLKS 675
 QY 580 MSE-----PRISGNDALM-----PSLTETKTVELLPVNG 611
 DB 676 QVAEOOSQPTOSTSQAOQOQOEKSLPGKELGPDPAALVTANPMLTETKS----- 726
 QY 612 EESLIDLPWHSFGADSVANTENEPYDARPARADRGITTPRSGGLTNKKEISEVKM 671
 DB 727 EKDLDTE-----YGERVSTTVQVTLPTVDDAVORAVEDVA---VAHQDA 773
 QY 672 DAEFRHDSGEYEHQKLVF---FAEDVGSNK---GAILGLMGVYATVITLVML 723
 DB 774 EPQOVHFMTHDGHRSSPSLRFEAQHNAKESGRNYFTLSFGAILMAVFPGVAVA 833
 QY 724 KKQKTSIH-HGVVEVDAVTP-----EERLSKMOONGYENPYKFFE 766
 DB 834 KMRTRSPPHAGFIEVDQVYTHHPIVREKIVPMNQINGENPYKFFE 883
 RESULT 14
 S38344
 CDEI-binding protein - mouse (fragment)
 Species: Mus musculus (house mouse)
 Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 03-May-1996
 C:Accession: S38344
 R:Hanes, J.; von der Kammer, H.; Kristjansson, G.I.; Schelt, K.H.
 Biochim. Biophys. Acta 1216, 154-156, 1993
 A:Title: The complete cDNA coding sequence for the mouse CDEI binding protein.
 A:Reference number: S38344; MUID:94032480
 A:Accession: S38344
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-246 <HAN>
 A:Cross-references: EMBL:Z22592
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 17.4%; Score 706; DB 2; Length 246;
 Best Local Similarity 51.5%; Pred. No. 5.1e-31;
 Matches 136; Conservative 35; Mismatches 51; Indels 42; Gaps 7;

QY 5 LALLIAAMTARALEV-----PTDGNAG---LAPQIAMEGRLNMHNVONGKMDSDP 56
 DB 15 LVLVLLGLTAPAAALAGTIEALANAGTFAVAPQIAMLGKLMHVNITQTKNEPDP 74
 QY 57 SCTKTCIDTKEGILOYCOEYPELOITNVVEANOPVTIQQMCKRGKCKOCTHPHFVPIYR 116
 DB 75 TGTGSLGTHKEEVLOYCOEYPELOITNVMEANQPVNIDSMCRDRCKS--HIVDPFK 132

QY 117 CLVGEVSDALLVPCKEFLHOERMDVCETHLHMHTVAKETCEKSTNLHDYGMLLPGCI 176
 DB 133 CLVGEFVSDVLLVPDNCFFHOERMEVECKHORHTLVKACLTGTLVISTGMLLPGCV 192
 QY 177 DKFRGVEFVCCPLAEESDNDVSDAEEDSDVMWGAOTDYADGSEDKVVEVAEEVEYAE 236
 DB 193 DQFHGTVEVCCP---QTKTVDS-----DSTMKEEEEEE--- 222
 QY 237 VEEEDADDED-DEDDGEVEEBAE 259
 DB 223 -EEDEDEDEEDYDLDKSEFPTEAD 245
 RESULT 15
 A32282
 Alzheimer's disease amyloid beta protein precursor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Aug-1989 #sequence_revision 17-Aug-1989 #text_change 13-Aug-1999
 C:Accession: A32282
 R:Yanada, T.; Sasaki, H.; Dohura, K.; Goto, I.; Sakaki, Y.
 Biochem. Biophys. Res. Commun. 158, 906-912, 1989
 A:Title: Structure and expression of the alternatively-spliced forms of mRNA for the
 A:Reference number: A32282; MUID:89149813
 A:Accession: A32282
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-100 <YAM>
 A:Cross-references: GB:M24397; NID:g200350; PIDN:AAA39929.1; PID:g200351
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing
 F:11-61/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
 Query Match 12.3%; Score 501; DB 2; Length 100;
 Best Local Similarity 92.0%; Pred. No. 1.6e-20;
 Matches 92; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 281 ESVEEVREVCSEQAETGPCRAMISRMYEDVTEGCAPEFYGGCGGNRNNDTEECMAV 340
 DB 1 ESVEEVREVCSEQAETGPCRAMISRMYFDYTEGKCVFFYGGCGGNRNNDTEECMAV 60
 QY 341 CGSAMSGSLKTTQEPPLARDPVKLTPTAASPDPAVDKYLE 380
 DB 61 CGSVSTQSLKTTSEPLRPQDDKLTPTAASPDPAVDKYLE 100

Search completed: October 31, 2002, 10:13:05
 Job time : 36.3075 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:55 ; Search time 17.048 Seconds
(without alignments)
1748.833 Million cell updates/sec

Title: US-09-785-215-2
Perfect score: 4058
Sequence: 1 MLEPGLALLLAAMTARALEV.....KMOQNGYENPYKFEQOMON 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	4058	100.0	770 1 A4_HUMAN	P05067 homo sapien
2	3937	97.0	770 1 A4_RAT	P08592 rattus norv
3	3927	96.8	770 1 A4_MOUSE	P13023 mus musculu
4	3921.5	96.6	751 1 A4_SAISC	O95241 salmirt sci
5	1981.5	48.8	763 1 APP2_HUMAN	O06481 homo sapien
6	1971.5	48.6	765 1 APP2_RAT	P15943 rattus norv
7	1704.5	42.0	695 1 APP2_MOUSE	O06335 mus musculu
8	1155.5	28.5	650 1 APP1_HUMAN	P03157 homo sapien
9	1150.5	28.4	653 1 APP1_MOUSE	O03157 mus musculu
10	737.5	18.2	886 1 A4_DROME	P14599 drosophila
11	457	11.3	87 1 A4_MACFA	P35601 macaca fasc
12	403	9.9	76 1 A4_MACMU	P23216 macaca mula
13	292	7.2	59 1 A4_BOVIN	O28053 bos taurus
14	288	7.1	58 1 A4_RABIT	O28748 oryctolagus
15	288	7.1	58 1 A4_SHEEP	O28757 ovitis aries
16	287	7.1	58 1 A4_CANEA	O28280 canis famli
17	283	7.0	57 1 A4_PIG	O28023 sus scrofa
18	283	7.0	57 1 A4_PIG	O28149 ursus marit
19	194.5	4.8	3911 1 A4_URSWA	O09996 h-a-kinase
20	186	4.6	252 1 SP22_HUMAN	O43291 homo sapien
21	186	4.6	993 1 SCPI_MOUSE	O62209 mus musculu
22	176	4.3	55 1 ISH1_STOHE	P31713 stoichiactis
23	175.5	4.3	579 1 G160_HUMAN	O08378 homo sapien
24	175	4.3	302 1 TPPI_RAT	O02445 rattus norv
25	174.5	4.3	252 1 SP22_MOUSE	O09u03 mus musculu
26	174.5	4.3	513 1 SP21_HUMAN	O43278 homo sapien
27	169	4.2	1875 1 MLEP1_YEAST	O02455 saccharomyc
28	168	4.1	304 1 TPPI_HUMAN	P16062 homo sapien
29	166	4.1	55 1 ISH2_STOHE	P81129 stoichiactis
30	164.5	4.1	507 1 SP1_MOUSE	O97097 mus musculu
31	163.5	4.0	346 1 AMBP_MERON	O65257 meriones un
32	163.5	4.0	1130 1 Y117_CAEEL	O11102 caenorhabdi
33	163	4.0	2944 1 CAL7_HUMAN	O02388 homo sapien

34	163	4.0	3176 1 CA36_HUMAN	P12111 homo sapien
35	162	4.0	304 1 TPPI_MACMU	O28864 macaca mula
36	162	4.0	407 1 IE68_HSVSA	O01062 herpesvirus
37	162	4.0	3137 1 CA36_CHICK	P15989 gallus galli
38	161.5	4.0	630 1 YCF2_OENVI	P13569 oenothera v
39	161.5	4.0	1278 1 DYNA_HUMAN	O14203 homo sapien
40	161	4.0	64 1 SPT3_HUMAN	P49223 homo sapien
41	160.5	4.0	721 1 YCF2_OENVI	P31568 oenothera p
42	160	3.9	802 1 NAB3_YEAST	P38996 saccharomyc
43	159	3.9	159 1 MCP1_MELCP	P82968 mellithaea c
44	158.5	3.9	2004 1 MOZ_HUMAN	O92794 homo sapien
45	158	3.9	58 1 ISIK_HELUPO	P00994 helix pomat

ALIGNMENTS

RESULT 1
ID A4_HUMAN STANDARD: PRT: 770 AA.
AC P05067; P09000; Q16011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)
DE (PN-II) (APP1) [contains: Beta-amyloid protein (Beta-Ap) (A-beta)].
GN APP OR A4 OR CVAP OR ADL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=871144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor."
RL Nature 325:733-736(1987).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors."
RL Nature 331:525-527(1988).
[3]
RN SEQUENCE FROM N.A.
RP MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Multhaup H. B.;
RT "The Pread(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons."
RL Nucleic Acids Res. 17:517-522(1989).
[4]
RN SEQUENCE FROM N.A.
RP MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukuhara F., Furuhata Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 500 kb region of human APP locus."
RL Nucleic Acids Res. 25:1802-1808(1997).
[5]
RN SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RP MEDLINE=88122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lampert E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease."
RL Nature 331:528-530(1988).

- [6]
RA SEQUENCE OF 287-367 FROM N.A.
RP MEDLINE=88122641; PubMed=2893291;
RX Kiteguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.,
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RL protease inhibitory activity.";
RN Nature 331:530-532(1988).
[7]
RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
RX MEDLINE=87231971; PubMed=3035554;
RA Robkis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.,
RT "Molecular cloning and characterization of a cDNA encoding the
RL cerebrovascular and the neuritic plaque amyloid peptides.";
RN Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
[8]
RP SEQUENCE OF 507-770 FROM N.A.
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RL Marotta C.A.,
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RL disease brain: coding and noncoding regions of the fetal precursor
RN mRNA are expressed in the cortex.";
RN Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
[9]
RP SEQUENCE OF 672-681.
RX MEDLINE=88035004; PubMed=3312495;
RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RT Tourtelotte W.W., Huebner V., Shively J.E.,
RL "Amyloid angiopathy of Alzheimer's disease: amino acid composition
RT and partial sequence of a 4,200-dalton peptide isolated from cortical
RL microvessels.";
RN J. Neurochem. 49:1394-1401(1987).
[10]
RP SEQUENCE OF 739-770 FROM N.A.
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikawa S.-I., Sasaki H., Don-ura K., Furuya H., Sakaki Y.,
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RL Gene 87:257-263(1990).
[11]
RP SEQUENCE OF 1-10 FROM N.A.
RX TISSUE=Liver;
RL MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.,
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
[12]
RP SEQUENCE OF 18-50.
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.,
RT "Purification of protease nexin II from human fibroblasts.";
RN J. Biol. Chem. 262:8508-8514(1987).
[13]
RP IDENTITY OF APP WITH NEXIN-II.
RX MEDLINE=89384866; PubMed=2506449;
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
RL Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
RA Slinn S.,
RT "The secreted form of the Alzheimer's amyloid precursor protein with
RL the Kunitz domain is protease nexin-II.";
RN Nature 341:144-147(1989).
[14]
RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
RX MEDLINE=90211252; PubMed=1969731;
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.,
RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
RL disease amyloid protein precursor.";
RN Biochem. Biophys. Res. Commun. 167:716-721(1990).
[15]
RP COMPLEX WITH G(O).
RX MEDLINE=93186965; PubMed=8446172;
RA Nishimoto I., Okamoto T., Matsura Y., Takahashi S., Okamoto T.,
RT Murayama Y., Ogata E.,
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
RL protein G(O).";
RN Nature 362:75-79(1993).
[16]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
RX MEDLINE=99215582; PubMed=10201399;
RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinsty W.J.,
RL Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
RA Parker M.W.,
RT "Crystal structure of the N-terminal, growth factor-like domain of
RL Alzheimer amyloid precursor protein.";
RN Nat. Struct. Biol. 6:327-331(1999).
[17]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
RX MEDLINE=91104913; PubMed=2125487;
RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.,
RT "X-ray crystal structure of the protease inhibitor domain of
RL Alzheimer's amyloid beta-protein precursor.";
RN Biochemistry 29:10018-10022(1990).
[18]
RP STRUCTURE BY NMR OF 289-344.
RX MEDLINE=92031488; PubMed=1718421;
RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
RL Kamarcik M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
RA Tamburini P.P.,
RT "Sequential NMR resonance assignment and structure determination of
RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
RL precursor protein.";
RN Biochemistry 30:10467-10478(1991).
[19]
RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE=94281210; PubMed=7516706;
RA Talafous J., Marciniowski K.J., Klopman G., Zagorski M.G.,
RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
RN Biochemistry 33:7788-7796(1994).
[20]
RP STRUCTURE BY NMR OF 696-706.
RX MEDLINE=97128622; PubMed=8973180;
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.,
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
RL membrane-mimicking environment.";
RN Biochemistry 35:16094-16104(1996).
[21]
RP STRUCTURE BY NMR OF 672-711.
RX MEDLINE=96359783; PubMed=9693002;
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.,
RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
RL environment. Is the membrane-spanning domain where we think it is?";
RN Biochemistry 37:11064-11077(1998).
[22]
RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE=20400066; PubMed=10940222;
RA Poulsen S.-A., Watson A.A., Craik D.J.,
RT "Solution structures in aqueous SDS micelles of two amyloid beta
RL peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
RT site.";
RN J. Struct. Biol. 130:142-152(2000).
[23]
RP STRUCTURE BY NMR OF 681-706.
RX MEDLINE=20400066; PubMed=10940221;
RA Zhang S., Iwata K., Lachemann M.J., Peng J.W., Li S., Stimson E.R.,
RL Lu Y., Felix A.M., Maggioni J.E., Lee J.P.,
RT "The Alzheimer's peptide beta adopts a collapsed coil structure in
RL water.";
RN J. Struct. Biol. 130:130-141(2000).
[24]
RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
RX MEDLINE=88296437; PubMed=2900137;
RA Dyrks T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
RL Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.,
RT "Identification, transmembrane orientation and biogenesis of the
RL amyloid A precursor of Alzheimer's disease.";

Query Match 100.0% Score 4058; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 2,6e-204;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGALALLLAAVTARALVPTDNGNGLAEPQIAWFCGRLLNNHNNVNGKMDSPSGTK 60
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QY 61 TCIDTKEGILQYCEVEYPELQITNVVEANQPTIQMWCKRGRKCKTNPHEVYPRCLVG 120
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QY 121 EYVSALLLVDPCKFLHQRMDVCEHLMHTYAKTCEKSTNLDYGMLLPCGDKRR 180
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QY 241 EADDEDEDGDBEEEAEPYEATERTTSTATTTTTSVEEYVREVCSEQAEFGPC 300
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QY 301 RAMISWYFDVTEGKCAPFYGGCGGNRNPTDEECMAVCSAMSQSLKTQEPALD 360
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QY 361 PKLPTASTPDVAVKYETPGDENEHAFQAKERLAKHERMSQVREWEAEERQA 420
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QY 421 KMLPKAKAVIQHEQEKVESLEQEAANERQOLVETHMAVEMALNDRRLALENYTAL 480
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 DB 421 KMLPKAKAVIQHEQEKVESLEQEAANERQOLVETHMAVEMALNDRRLALENYTAL 480
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QY 481 QAVPRPRRVRNMLKKYVAEOKDRQHTLKHPRVBMVDPKRAAQRSQVNHRLRYER 540
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QY 541 MNGSILYNVAEIEIDVEDELQKQNTSDVLANMISEPRISYNDALMPSLTET 600
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QY 601 KTTVELLPVNGEFSDDLQPMHSFGADSVPAANTENEVEPVDAAPADRLTTRPGSLTN 660
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QY 661 ITTEISEVKMDAEFRHDSGEYEHQKLFPAEDVGSNNKGAITGLWGVVATVITL 720
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QY 721 VMLKKQYTSIHGGVEVDAVTPREERHLSKMQONGYENPTYKFFEQMON 770
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 DB 721 VMLKKQYTSIHGGVEVDAVTPREERHLSKMQONGYENPTYKFFEQMON 770
 |||||

RESULT 2
 A4_RAT STANDARD; PRT; 770 AA.
 AC P08592;
 DT 01-AUG-1988 (rel. 08, Created)
 DT 01-DEC-1992 (rel. 24, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein, homolog precursor
 DE (Amyloidogenic glycoprotein) (AG).
 GN APP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]

RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=88312583; PubMed=2900758;
 RA Shivers B.D., Hillich C., Multhaup G., Salbaum J.M., Beyreuther K.,
 RA Seeburg P.H.;
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
 RT in rat brain suggests a role in cell contact.";
 RL EMBO J. 7:1365-1370(1988).
 RN [2]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89183625; PubMed=2648331;
 RA Kang J., Mueller-Hill B.;
 RT "The sequence of the two extra exons in rat preA4.";
 RL Nucleic Acids Res. 17:2130-2130(1989).
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -I- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -I- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11 ALPHA, BETA, AND GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -I- SIMILARITY: CONTRAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC -----
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 CC -----
 CC EMBL: X07648; CA30488.1; -;
 CC EMBL: X14066; CA32229.1; -;
 CC PIR: S00550; S00550.
 CC PIR: S03607; S03607.
 CC HSP: P05067; IAA.
 CC DR HSSE; P05067; IAA.
 CC DR InterPro: IPR001868; A4_APP.
 CC DR InterPro: IPR002223; Kunitz_BPTI.
 CC DR Pfam: PF02177; A4_EXTRA; 1.
 CC DR Pfam: PF00014; Kunitz_BPTI; 1.
 CC DR PRINTS; PR00203; AMYLOIDA4.
 CC DR PRINTS; PR00759; BASICPTASE.
 CC DR SMART; SM00006; A4_EXTRA; 1.
 CC DR SMART; SM00131; KU; 1.
 CC DR PROSITE; PS00319; A4_EXTRA; 1.
 CC DR PROSITE; PS00320; A4_INTRA; 1.
 CC DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 CC DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 CC DR Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 CC KW Alternative splicing; Serine
 CC FT SIGNAL 1 17
 CC FT CHAIN 18 770
 FT
 FT DOMAIN 18 699
 FT TRANSMEM 700 723
 FT DOMAIN 724 770
 FT DOMAIN 673 715
 FT DOMAIN 287 345
 FT SITE 759 762
 FT DISULFID 291 341
 FT DISULFID 300 324
 FT DISULFID 316 337
 FT CARBOHYD 542 542
 FT CARBOHYD 571 571
 FT VARSPLIC 289 289
 FT VARSPLIC 290 364
 FT VARSPLIC 364 364
 FT SEQUENCE 770 AA; 86704 MW; C26C906B82929A7 CRC64;
 Query Match 97.0%; Score 3937; DB 1; Length 770;

Best Local Similarity 96.9%; Pred. No. 5, 2e-198;
Matches 746; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

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OY 1 MPRGLALLLAAANTARALVPTDGNGLLAEPQIAFCGRLLNNHNVQNGKSDSPSGTK 60
DB 1 MPRSLALLLAAANTARALVPTDGNGLLAEPQIAFCGRLLNNHNVQNGKSDSPSGTK 60
OY 61 TCIDTREGILQYCOEYVPELQITNVANOPVITQNMCKRGKRGKCTHHPFYRQCGLG 120
DB 61 TCIGTREGILQYCOEYVPELQITNVANOPVITQNMCKRGKRGKCTHHPFYRQCGLG 120
OY 121 EFVSADLALVPRCKFLHQRMDVCEHLMHTYAKETCESEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSADLALVPRCKFLHQRMDVCEHLMHTYAKETCESEKSTNLHDYGMLLPCGIDKFR 180
OY 181 GVEFYCCPLAESDNDVSDAEEDSDVWVGADTDYADGCGEDKVEVAEEBEVADVEE 240
DB 181 GVEFYCCPLAESDNDVSDAEEDSDVWVGADTDYADGCGEDKVEVAEEBEVADVEE 240
OY 241 EADDDDDDDGDEVEEAEPEYEATERTSTATTTTTSVEEYVREVCSPQATGTC 300
DB 241 EADDDDDDDGDEVEEAEPEYEATERTSTATTTTTSVEEYVREVCSPQATGTC 300
OY 301 RAMISRWYEDVTEGKCAPEFYGGCGGNRNFTDEEYCMACVCSGMSQSLKTQOEPFLAD 360
DB 301 RAMISRWYEDVTEGKCAPEFYGGCGGNRNFTDEEYCMACVCSGMSQSLKTQOEPFLAD 360
OY 361 PKRLPTASTDADVDTKETPDDENEHNAHFOKAKERLAKHRRRSQVREBEAERQA 420
DB 361 PKRLPTASTDADVDTKETPDDENEHNAHFOKAKERLAKHRRRSQVREBEAERQA 420
OY 421 KMLPRADKAVIYQHOEKESLEQEAANRQOLVETNMAVREMLDRRLALENTAL 480
DB 421 KMLPRADKAVIYQHOEKESLEQEAANRQOLVETNMAVREMLDRRLALENTAL 480
OY 481 QAVPRPRHVENMLKKYVAEOKROHTLKEHVRVMDPKKAQIRSOVMTHLRVYER 540
DB 481 QAVPRPRHVENMLKKYVAEOKROHTLKEHVRVMDPKKAQIRSOVMTHLRVYER 540
OY 541 MNOSLSLVNVAVAEIOEDVDELQKONYSDVLANMISPRISYNDALMPSLTET 600
DB 541 MNOSLSLVNVAVAEIOEDVDELQKONYSDVLANMISPRISYNDALMPSLTET 600
OY 601 KTTVELLPNGESLDDLOPMHSGADSVPAANTENEVEVDARPADRLTTPGSGLTN 660
DB 601 KTTVELLPNGESLDDLOPMHSGADSVPAANTENEVEVDARPADRLTTPGSGLTN 660
OY 661 IKTEISEVKMDAEFRHDSGYEVHOKLVFAEDVGSNKGATIGLVGGVATVITVL 720
DB 661 IKTEISEVKMDAEFRHDSGYEVHOKLVFAEDVGSNKGATIGLVGGVATVITVL 720
OY 721 VLKKKQYTSIHGGVVEVDAATPRERHLSKMOQNGYENPTKFFROMON 770
DB 721 VLKKKQYTSIHGGVVEVDAATPRERHLSKMOQNGYENPTKFFROMON 770

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RESULT 3

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A4_MOUSE STANDARD: PRT: 770 AA.
ID A4_MOUSE
AC P12023;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (Ag).
GN App.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N. A.
RC STRAIN-BALB/C; TISSUE=Brain;

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RX MEDLINE=92096458; PubMed=1756177;
RA de Strooper B., van Leuven F., van den Bergh H.;
RT "The amyloid beta protein precursor or proteinase nexin II from mouse
RL Biochim. Biophys. Acta 1129:141-143(1991).
RN [12]
RP SEQUENCE OF 1-289 AND 365-770 FROM N. A.
RC TISSUE=Brain;
RX MEDLINE=88106489; PubMed=3322280;
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
RN [13]
RP REVISIONS.
RA Yamada T.;
RL Submitted (MAR-1988) to the EMBL/Genbank/DBJ databases.
RN [14]
RP SEQUENCE OF 289-364 FROM N. A.
RC STRAIN=CD-1; TISSUE=Placenta;
RX MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RL precursor of Mus domesticus."
RN Nucleic Acids Res. 17:5396-5396(1989).
RN [15]
RP SEQUENCE OF 1-19 FROM N. A.
RX MEDLINE=92209998; PubMed=1555768;
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RL Alzheimer's disease amyloid precursor-encoding gene in mouse."
RN Gene 112:189-195(1992).
RN [16]
RP SEQUENCE OF 281-380 FROM N. A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain, and Kidney;
RX MEDLINE=89149813; PubMed=2493250;
RA Yamada T., Sasaki H., Dohtu K., Goto I., Sasaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RL for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor."
RN Biochem. Biophys. Res. Commun. 158:906-912(1989).
RL -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
CC LIVER.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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CC
CC EMBL: X59379; ?; NOT ANNOTATED_CDS.
CC EMBL: M18373; AAA37139.1; ?
CC EMBL: X15210; AAA33280.1; ?
CC EMBL: D10603; BAA01456.1; ?
CC EMBL: M24397; AAA39929.1; ?
CC PIR: A27485; A27485.
CC PIR: S04855; S04855.
CC PIR: S19727; S19727.

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DR HSSP; P05067; 100M.
 DR MGD; MGI:88059; APP.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00177; A4_EXTRA; 1.
 DR Pfam; PF0014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOID4.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 DR Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17
 FT CHAIN 18 770
 FT TRANSMEM 18 699
 FT DOMAIN 700 723
 FT DOMAIN 724 770
 FT DOMAIN 673 715
 FT DOMAIN 287 345
 FT SITE 759 762
 FT DISULFID 291 341
 FT DISULFID 300 324
 FT DISULFID 316 337
 FT CARBOHYD 542 542
 FT CARBOHYD 571 571
 FT VASPLIC 289 289
 FT VASPLIC 290 364
 FT VASPLIC 346 380
 SQ SEQUENCE 770 AA; 86752 MW; 26C50DE089C6AFAA CRC64;
 Query March 96.8%; Score 3927; DB 1; Length 770;
 Best Local Similarity 96.8%; Pred. No. 1.7e-197;
 Matches 745; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 MPEGLALLLAAMTARALEVPTDNGAGLLAEPOIAMFCGRLLMHNVNQNGKWDSPSGTK 60
 DB 1 MPEGLALLLAAMTARALEVPTDNGAGLLAEPOIAMFCGRLLMHNVNQNGKWDSPSGTK 60
 QY 61 TCIDKEGILLQCCVEYELDTTNNVEANOPTIOMCKRGKCKOCTHPIFYRCVIG 120
 DB 61 TCIDKEGILLQCCVEYELDTTNNVEANOPTIOMCKRGKCKOCTHPIFYRCVIG 120
 QY 121 EFVSDALLVPDKCKFLHOBEMDVCEHLMHTVAKETCSSEKSTNLHDYGMLLPGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHOBEMDVCEHLMHTVAKETCSSEKSTNLHDYGMLLPGIDKFR 180
 QY 121 EFVSDALLVPDKCKFLHOBEMDVCEHLMHTVAKETCSSEKSTNLHDYGMLLPGIDKFR 180
 DB 121 EFVSDALLVPDKCKFLHOBEMDVCEHLMHTVAKETCSSEKSTNLHDYGMLLPGIDKFR 180
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 DB 181 GVEFYCCPLAEESNDVSDAEEDSDVWVGADTDVADGSDKVEVAEEVEEVEEVEE 240
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 DB 241 EADDEDDEDDEVEEAEPEEATEERTSTATTTTTSVEVEVEVEVEVEVEVEVE 300
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 QY 301 RAMISRMWFEVTEGKCAFFYGGCGGNRNPFDETEYCAVCGSVSTGLTKTSTPLPD 360
 DB 301 RAMISRMWFEVTEGKCAFFYGGCGGNRNPFDETEYCAVCGSVSTGLTKTSTPLPD 360
 QY 361 PVKLEPTAASPDVADKLETPGDENEHAHFOKAKERLEAKIREMSOVMEAEAEQA 420
 DB 361 PVKLEPTAASPDVADKLETPGDENEHAHFOKAKERLEAKIREMSOVMEAEAEQA 420
 QY 361 PVKLEPTAASPDVADKLETPGDENEHAHFOKAKERLEAKIREMSOVMEAEAEQA 420
 DB 361 PVKLEPTAASPDVADKLETPGDENEHAHFOKAKERLEAKIREMSOVMEAEAEQA 420
 QY 421 KNLPRADKAAVIOHFOEYVESLEOEAANEROOLVETIHARVAMLNDRRRLALEVYITL 480
 DB 421 KNLPRADKAAVIOHFOEYVESLEOEAANEROOLVETIHARVAMLNDRRRLALEVYITL 480
 QY 421 KNLPRADKAAVIOHFOEYVESLEOEAANEROOLVETIHARVAMLNDRRRLALEVYITL 480
 DB 421 KNLPRADKAAVIOHFOEYVESLEOEAANEROOLVETIHARVAMLNDRRRLALEVYITL 480
 QY 481 QAVPRPRHVEVNMKKYVAEOKDRQHTLKHFEHVMVDPKAAQIRSOVMTLHVIYER 540
 DB 481 QAVPRPRHVEVNMKKYVAEOKDRQHTLKHFEHVMVDPKAAQIRSOVMTLHVIYER 540

DB 481 QAVPRPRHVEVNMKKYVAEOKDRQHTLKHFEHVMVDPKAAQIRSOVMTLHVIYER 540
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 DB 541 MNOSLSLYNPAYAAEELQDEVDLQEKQYSDVLANMISERISYGNALMPSLRET 600
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 DB 601 KTYVELLPVNGEFLDDQPMHSGADSVPAANTEVEVPVAPADGLTTRPGSGLTN 660
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 DB 661 IKTEIESEVKMDAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMGVYATVYITL 720
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 DB 721 VMLKKOYTSIHGVEYVDAAVTPBERLSKMOONGYENPYKFFEQMON 770
 RESULT 4
 A4_SAISC STANDARD; PRT; 751 AA.
 AC Q95241;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-amyloid protein (Beta-Ap) (A-beta)].
 GN APP.
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver, and Kidney;
 RX MEDLINE=96108492; PubMed=8532114;
 RA Ley E., Amorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy."
 RL Neurobiol. Aging 16:805-808(1995).
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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 CC EMBL; S81024; AAD14347.1; .
 DR HSSP; P05067; 1AAP.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00177; A4_EXTRA; 1.
 DR Pfam; PF0014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOID4.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_INTRA; 1.
 DR PROSITE; PS00320; A4_EXTRA; 1.

DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
 KW Signal; Serine protease inhibitor.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 751 A4 PROTEIN.
 FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 681 704 POTENTIAL.
 FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
 FT SITE 740 743 CLATERIN-BINDING (BY SIMILARITY).
 FT ACT_SITE 301 302 REACTIVE BOND.
 FT DISULFID 291 341 BY SIMILARITY.
 FT DISULFID 300 324 BY SIMILARITY.
 FT DISULFID 316 337 BY SIMILARITY.
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
 SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 96.6%; Score 3921.5; DB 1; Length 751;
 Best Local Similarity 96.9%; Pred. No. 3.2e-197;

Matches 746; Conservative 2; Mismatches 3; Indels 19; Gaps 1;

QY 1 MDPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLLMHNHNVONGKNDSPSGTK 60
 1 MDPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLLMHNHNVONGKNDSPSGTK 60
 DB 1 MDPGALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLLMHNHNVONGKNDSPSGTK 60
 QY 61 TCIDTFREGILQCYQEVYPELQITNVANQVPTIONMCKRGKRGKTHPEVYPRCLVG 120
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 121 EYVSALLVPDCKLHORMDVCEHLHMHVAKETSEKSTNLDGMLPGCIDKFR 180
 DB 121 EYVSALLVPDCKLHORMDVCEHLHMHVAKETSEKSTNLDGMLPGCIDKFR 180
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 181 GVEFYCCPLAESDNDVSDAEDSDVWVGADPYADGSDKVVVEAEVEEVEE 240
 DB 181 GVEFYCCPLAESDNDVSDAEDSDVWVGADPYADGSDKVVVEAEVEEVEE 240
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 DB 181 GVEFYCCPLAESDNDVSDAEDSDVWVGADPYADGSDKVVVEAEVEEVEE 240
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 301 RAMISRWEDVDEGCAPEFYGGCGNNRNPTEECYCAVGSANSQSILKTQGPLARD 360
 DB 301 RAMISRWEDVDEGCAPEFYGGCGNNRNPTEECYCAVGSANSQSILKTQGPLARD 360
 QY 361 PVKLEPTTAAPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVAREMEAEQA 420
 361 PVKLEPTTAAPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVAREMEAEQA 420
 DB 361 PVKLEPTTAAPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVAREMEAEQA 420
 QY 345 ---IPTTAAPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVAREMEAEQA 401
 345 ---IPTTAAPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVAREMEAEQA 401
 DB 345 ---IPTTAAPDAVDKYLETPGDENEHAFQAKERLEAKHREMSQVAREMEAEQA 401
 QY 421 KMLPRADKKAIVQHOEKEVESLEQEAANEQOVLVETHARVEMLNDRRRLALENYTAL 480
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 DB 421 KMLPRADKKAIVQHOEKEVESLEQEAANEQOVLVETHARVEMLNDRRRLALENYTAL 480
 QY 402 KMLPRADKKAIVQHOEKEVESLEQEAANEQOVLVETHARVEMLNDRRRLALENYTAL 461
 402 KMLPRADKKAIVQHOEKEVESLEQEAANEQOVLVETHARVEMLNDRRRLALENYTAL 461
 DB 402 KMLPRADKKAIVQHOEKEVESLEQEAANEQOVLVETHARVEMLNDRRRLALENYTAL 461
 QY 481 QAVPRPRHVFEMLKYYRAEQKROHILKHEHVRMVDPKKAADIRSVYHLEVIYER 540
 481 QAVPRPRHVFEMLKYYRAEQKROHILKHEHVRMVDPKKAADIRSVYHLEVIYER 540
 DB 481 QAVPRPRHVFEMLKYYRAEQKROHILKHEHVRMVDPKKAADIRSVYHLEVIYER 540
 QY 462 QAVPRPRHVFEMLKYYRAEQKROHILKHEHVRMVDPKKAADIRSVYHLEVIYER 521
 462 QAVPRPRHVFEMLKYYRAEQKROHILKHEHVRMVDPKKAADIRSVYHLEVIYER 521
 DB 462 QAVPRPRHVFEMLKYYRAEQKROHILKHEHVRMVDPKKAADIRSVYHLEVIYER 521
 QY 541 MNQSLSLLYNPAAVEEIQDEVDLQEQNSDDVLANMISEPRTSYGNDLMSLETET 600
 541 MNQSLSLLYNPAAVEEIQDEVDLQEQNSDDVLANMISEPRTSYGNDLMSLETET 600
 DB 541 MNQSLSLLYNPAAVEEIQDEVDLQEQNSDDVLANMISEPRTSYGNDLMSLETET 600
 QY 522 MNQSLSLLYNPAAVEEIQDEVDLQEQNSDDVLANMISEPRTSYGNDLMSLETET 581
 522 MNQSLSLLYNPAAVEEIQDEVDLQEQNSDDVLANMISEPRTSYGNDLMSLETET 581
 DB 522 MNQSLSLLYNPAAVEEIQDEVDLQEQNSDDVLANMISEPRTSYGNDLMSLETET 581
 QY 601 KTTVELLYNGEFSLDDIQPHHSFGADSVPAANTEVEVVDARPAADRGTLTPSGSLTN 660
 601 KTTVELLYNGEFSLDDIQPHHSFGADSVPAANTEVEVVDARPAADRGTLTPSGSLTN 660
 DB 601 KTTVELLYNGEFSLDDIQPHHSFGADSVPAANTEVEVVDARPAADRGTLTPSGSLTN 660
 QY 582 KTTVELLYNGEFSLDDIQPHHSFGADSVPAANTEVEVVDARPAADRGTLTPSGSLTN 641
 582 KTTVELLYNGEFSLDDIQPHHSFGADSVPAANTEVEVVDARPAADRGTLTPSGSLTN 641
 DB 582 KTTVELLYNGEFSLDDIQPHHSFGADSVPAANTEVEVVDARPAADRGTLTPSGSLTN 641
 QY 661 IKTEIISEYKMDAEPFRHSGYEVHOKLVFADYGSNKGAITGLMVGVAIVATIVITL 720
 661 IKTEIISEYKMDAEPFRHSGYEVHOKLVFADYGSNKGAITGLMVGVAIVATIVITL 720
 DB 661 IKTEIISEYKMDAEPFRHSGYEVHOKLVFADYGSNKGAITGLMVGVAIVATIVITL 720
 QY 642 IKTEIISEYKMDAEPFRHSGYEVHOKLVFADYGSNKGAITGLMVGVAIVATIVITL 701
 642 IKTEIISEYKMDAEPFRHSGYEVHOKLVFADYGSNKGAITGLMVGVAIVATIVITL 701
 DB 642 IKTEIISEYKMDAEPFRHSGYEVHOKLVFADYGSNKGAITGLMVGVAIVATIVITL 701
 QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQQNGYENPTYKFEQMON 770
 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQQNGYENPTYKFEQMON 770
 DB 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQQNGYENPTYKFEQMON 770

DB 702 VMLKKQYTSIHGVEVDAVTPPEERHLSKMQQNGYENPTYKFEQMON 751
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 5
 APP2_HUMAN STANDARD; PRT; 763 AA.
 ID APP2_HUMAN
 AC 006481.
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH)
 DE (CDEI-box binding protein) (CDEBP).
 GN APP2 OR APP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RX MEDLINE=93250009; PubMed=8485127;
 RA Sprecher C.A., Grant F.J., Grimm G., O'Hara P.J., Norris F.,
 RA Norris K., Foster D.C.;
 RT "Molecular cloning of the cDNA for a human amyloid precursor protein
 RT homolog: evidence for a multigene family.";
 RL Biochemistry 32:4481-4486(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RX MEDLINE=95217334; PubMed=7702756;
 RA von der Kammer H., Hanes J., Klaiding J., Scheit K.H.;
 RT "A human amyloid precursor-like protein is highly homologous to a
 RT mouse sequence-specific DNA-binding protein.";
 RL DNA Cell Biol. 13:1137-1143(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=94035131; PubMed=8220435;
 RA Wasco W., Gurubhagavata S., Paradis M., Romano D.M., Sisodia S.S.,
 RA Hyman B.T., Neve R.L., Tanzi R.E.;
 RT "Isolation and characterization of APP2 encoding a homologue of the
 RT Alzheimer's associated amyloid beta protein precursor.";
 RL Nat. Genet. 5:95-99(1993).
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF HEMOSTASIS. THE
 CC SOLUBLE FORM MAY HAVE INHIBITORY PROPERTIES TOWARDS COAGULATION
 CC FACTORS. MAY INTERACT WITH CELLULAR G-PROTEIN SIGNALING PATHWAYS.
 CC MAY BIND TO THE DNA 5'-GTGACATG-3' (CDEI BOX).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
 CC (POTENTIAL).
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; 1 (SHOWN HERE), 2 AND
 CC 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: IN PLACENTA, BRAIN, HEART, LUNG, LIVER, KIDNEY
 CC AND ENDOTHELIAL TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: S60099; AAC60589.1; -;
 CC EMBL: L09209; AAA35526.1; -;
 CC EMBL: 222572; CA80295.1; -;
 CC EMBL: L27631; AAC41701.1; -;
 CC HSSP: P05067; IMP.
 CC MM: 104776; -;
 CC InterPro: IPR001868; A4_APP.
 CC InterPro: IPR002223; Kunitz_BPTI.
 DR

DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOID4.
 DR PRINTS: PR00759; BASICPASE.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
 DR Transmembrane; Signal; Alternative splicing; DNA-binding;
 KW Nuclear protein; Serine protease inhibitor.
 FT SIGNAL 1 29
 FT CHAIN 30 763
 FT DOMAIN 30 692
 FT TRANSMEM 693 716
 FT DOMAIN 717 763
 FT DOMAIN 215 280
 FT DOMAIN 306 364
 FT DOMAIN 215 231
 FT ACT_SITE 320 321
 FT DISULFID 310 360
 FT DISULFID 319 343
 FT DISULFID 335 356
 FT VARSPLIC 308 363
 FT VARSPLIC 613 624
 FT CONFLICT 543 543
 FT SEQUENCE 763 AA; 86955 MW; CA3AVD6DB8A28D0 CRC64;

Query March 48.8%; Score 1981.5; DB 1; Length 763;
 Best Local Similarity 50.4%; Pred. No. 3.2e-96;
 Matches 408; Conservative 127; Mismatches 166; Indels 107; Gaps 21;

QY 5 LALLLAATAAAEY-----PTDGNAG---LAEPOIAMFCGRILNMHNVONGKWDSDP 56
 DB 15 LLLLLVGLTAPALAGIYELALANAGTFAVAEPQIAMFCGRILNMHNVIGTKMEDP 74
 QY 57 SGTAKICITKEGILYOCGEVPELOITNVENANQYITONCKRRKQCKTTPHVIYIR 116
 DB 75 TGTAKCFETKEVLOYCOEMPELOITNVEMANQRYSDNMCRKCKOCKS--REVTPEK 132
 QY 117 CLVGEFVSDALLVPCKCFLEHMRDVCETHLHMTVAKETSEKSTNLHDGMLPGI 176
 DB 133 CLVGEFVSDVLLVPCKCFLEHMRDVCETHLHMTVAKETSEKSTNLHDGMLPGI 192
 QY 177 DKFRGVEVCCPLAEESNVDSADAEDSDVMWGADTDVAGSEDKVVEAEVEEYAE 236
 DB 193 DQFHGTEYVCCPQTKITIGSVKSEEEDEDE-----EEDEDEDEDDVYKSEPTED 245
 QY 237 VEE--EEA--DDEDEDEGDEVEEAE-----EPYEATERTSTATTITTTTSEYE 284
 DB 246 LEDFTEAVDDEDEDEEVEEVEEDRDYYTDFKGDYNE--ENPTEPSDGTMSDKET 303
 QY 285 EVFREVCSEQAEATGCRAMISRMYPDVTGKCAPEFFGCGGGRNNPFEYCAVCSA 344
 DB 304 HDKAVKVCQEAHTGCRAMVPMWYFDLSKGCYVRITIGGCGGGRNNPFESEDCMAVCSA 363
 QY 345 MSQSLIKTTQELPARDPVKLTPTAASPDVADKYLETDPDENEHNAHFOKAKERLEAKHRE 404
 DB 364 I-----PPIPLPT-----NDVDYFETSADNDENHARFOKAKQAKOLEIRRN 403
 QY 405 RMSQVMEEMEAERQAKNLPRKADKAVIQHPOEKVESLEQEAANRQOLVTHMARVEM 464
 DB 404 RMDKRVKKEEAELEQAKNLPRKAROTLLQHFAMKVALEKEKASERQOLVTHMARVEM 463
 QY 465 LNDRRRLALENTYALQAVPPRRHVFNNLKKYVRAEQRDQHTLKHENHVMVPKRAA 524
 DB 464 LNDRRRLALENTYALQAVPPRRHVFNNLKKYVRAEQRDQHTLKHENHVMVPKRAA 523
 QY 525 QIRSOVTHLAVIYERMNOSLSLNVPAVAEIEDEVELLOKBOYSDVLANMISEP 584
 DB 524 QMRSOVTHLAVIYERRNOSLSLNVPAVAEIEDEVELLOKBOYSDVLANMISEP 572

QY 585 RISYCNDAIMPSTETKTVELLPVNGEFSLDDLOPMHSGFADSVANTENEVEPDPAR 644
 DB 573 -----DQFTASISSTPVDV---VSSEES--EELPPFPF--HPPALPENE-----DTP 616
 QY 645 AADRGLTTPRSGGLTN-----IKTEE--ISEVKDAEFRHDSGYEHHOKLVFAEDVG 696
 DB 617 ELYHPM--KKSGVGEQDGLGAEKYNKSKNDKEMVNIQEDLV--KEMIFNAERVG 672
 QY 697 S-----NKGALIGLNGVYIATVITLMLKKKOTYSIHGVEVD 739
 DB 673 GLEERESVGLRDEFSLSALIGLTVIAVAIVISIVMLKRYGTISGIVEVD 732
 QY 740 AAVPPEERHLSKMQNGENPYPKFEOMO 769
 DB 733 PMLTPPEERHLMKNHNGENPYPKFEOMO 762
 (RESULT 6
 APP2_RAT STANDARD; PRT; 765 AA.
 AC P15943;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Amyloid-like protein 2 precursor (Sperm membrane protein YMK-II).
 GN APLP2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE OF 1-627 FROM N.A.
 RC STRAIN=Wistar; TISSUE=Brain, and Heart;
 RX MEDLINE=94368849; PubMed=8086458;
 RA Sandbriink R., Masters C.L., Beyreuther K.;
 RT "Complete nucleotide and deduced amino acid sequence of rat amyloid
 RT protein precursor-like protein 2 (APLP2/APPH): two amino acids length
 RT difference to human and murine homologues.";
 RL Biochim. Biophys. Acta 1219:167-170(1994).
 RN [2]
 RP SEQUENCE OF 575-765 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=90207205; PubMed=1690887;
 RA Yan Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
 RT "Characterization of cDNA encoding a human sperm membrane protein
 RT related to A4 amyloid protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS: A (SHOWN HERE), B, C AND D;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC
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 CC
 CC EMBL: X77934; CA54906.1; -;
 CC EMBL: M31322; AAA42352.1; -;
 CC PIR: A35981; A35981.
 CC HSSP: P05067; IAMP.
 CC InterPro: IPR001868; A4_APP.
 CC InterPro: IPR002223; Kunitz_BPTI.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC Pfam: PF00014; Kunitz_BPTI; 1.
 CC PRINTS: PR00203; AMYLOID4.
 CC PRINTS: PR00759; BASICPASE.
 CC SMART: SM00006; A4_EXTRA; 1.
 CC SMART: SM00131; KU; 1.

DR MGI: 88047; APL2.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA.
 DR SMART: SM0006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR Transmembrane; DNA-binding; Signal; Nuclear protein.
 FT SIGNAL 1 29
 FT CHAIN 30 695
 FT DOMAIN 30 624
 FT TRANSMEM 625 648
 FT TRANSMEM 649 695
 FT DOMAIN 218 294
 FT DOMAIN 218 231
 FT DOMAIN 236 266
 FT CARBOHYD 485 485
 FT CONFLICT 185 189
 FT SEQUENCE 695 AA; 78944 MW; BBF4B95AAB2A0311 CRC64;

Query Match 42.0%; Score 1704.5; DB 1; Length 695;
 Best Local Similarity 46.9%; Pred. No. 7.5e-82;
 Matches 371; Conservative 113; Mismatches 170; Indels 137; Gaps 24;

QY 5 LALLLAAMTARALEY-----PTDGNAG---LLAEPOIMFGRLNMHNNVNGKMDSDP 56
 DB 15 LVLVLLGLITAPAAAGTIEALANAGTGFVAEPQIMLCGLMHVNIOTGKWEPP 74
 QY 57 SGTGCTIDTKEGIIQYCEVPELOITNVANOPVITONMCKRGKCKCTPHFVPIYR 116
 DB 75 TGTGCTGKTEVLYQCEIYPELOITNVANOPVINDSMCRDCKRCKS--HVIYPERK 132
 QY 117 CLVGEFVSDALIVPKCKFLHOERMDVCTHLMHTVAKETSEKSTNHIDVGLLPGCI 176
 DB 133 CLVGEFVSDVLLVPPNCGFHOERMEVCKHORMHTLVKACLTGLTLYSGMLPGCV 192
 QY 177 DKFGEVEVCCPLAEESDNDADAEEDSDVMWGADIDVAGSDCKVVEVEEVEVAE 236
 DB 193 DQFHGEVYCCP---QTKVND-----DSYMSK-----EEEE--- 221
 QY 237 VEEEAADDEDEDEDEVEEAEPEEYEAETETTSIATTTTTSVEEVEVREVCSEAE 296
 DB 222 -EEDEEEDDEEDYLDKSEFPTEADLEPTE---AADEEEDDEEGERVED----- 270
 QY 297 TGPCRAMISRWYEDYTEGCAPFEYGGCGGNRNNFDTEYCAVAGSANSQSLTKTQEP 356
 DB 271 -----RDYTD-----PF-----KDDYNEENPTE-----PSSEGT--SDKE 301
 QY 357 LARDEVKLTPTAASPTDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMEWEA 416
 DB 302 LVHD-VKVPPTPLPTND-VDYVLETSADNENHARFQAKAEQLEIRHRNMDKVKEMEA 359
 QY 417 EROAKNLEKADKAVIOHFOEKVESLEOPANEKOOLVETHMARVEMLNDRRALALENY 476
 DB 360 ELQANLKEPTEKOTLHOFQAMVKALEKAEASEKOOLVETHLARVEMLNDRRALALENY 419
 QY 477 ITALQAVPRPHVFMKLVYRAEOKROHGLKHEHVRMDPKKAQIRSOVTHLRY 536
 DB 420 LAALQSDPPRRIRLOALRRVRAENKDLIRHIOHLAVDPKRAOMKSOVTHLHV 479
 QY 537 IYERNQSLILLYNPAVAEETODEVDELLOEKQNSDVLNMTSEPRISYGNALMPS 596
 DB 480 IEEERNQSLITLLYKVVAQETOEIEDLEQOR-----ADM-----DQFTSS 522
 QY 537 LTERITYELLVNGEFSLDLQPMHSGADSVRPANTEVEEPPVDARPAADGLTTRPGS 656
 DB 523 ISENVDVAVSESE-EIPEFPHLPF-----PSISENE-----GSGMAEOG- 565
 QY 657 GLTNKTEEI-SEVKMAEPRHDSGYEVHOKLVFAEDVGS-----N 698
 DB 566 GLIGEEKVINSKMDEMVMYIDETLDV--KEMITNAEVEGLLEEPSVGLREDFSLIS 623
 QY 699 KGATGLMVGAVTAVITVITLVMLKKROYTSIHGVEVVDAAVTPERRHLSKMOONGYE 758

DB 624 SNALGLLVIAINATVIVISLVMLKRYGTHSGIYEVDMLPPEERHLKMNHGYE 683
 QY 759 NPTKFEQMO 769
 DB 684 NPTKYLEQMO 694

RESULT 8
 APPL_HUMAN
 ID APPL_HUMAN STANDARD; PRT; 650 AA.
 AC P51693; O00113;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Amyloid-like protein 1 precursor (APLP1).
 GN APLP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxId:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98088960; PubMed=9428684;
 RA Paliga K., Peraus G., Kieger S., Duwrtwang U., Hesse L., Multhaup G.,
 Masters C.L., Beyreuther K., Weidemann A.;
 RT "Human amyloid precursor-like protein 1--cDNA cloning, ectopic
 expression in COS-7 cells and identification of soluble forms in the
 cerebrospinal fluid.";
 RL Eur. J. Biochem. 250:354-363(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98180887; PubMed=9521588;
 RA Lenkner U., Kestila M., Lamerdin J., McCreedy P., Adamson A.,
 RA Olsen A., Trygvason K.;
 RT "Structure of the human amyloid-precursor-like protein gene APLP1 at
 19q13.1.";
 RL Hum. Genet. 102:192-196(1998).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. C-TERMINALLY
 PROCESSED IN THE GOLGI COMPLEX AND IS THEN SECRETED.
 CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN, PARTICULARLY
 IN THE CEREBRAL CORTEX POSTSYNAPTIC DENSITY.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U48437; AAB96331.1;
 CC EMBL: AD000864; AAB50173.1;
 CC HSSP: P05067; JMKP.
 DR MIM: 104775; JMKP.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA.
 DR SMART: SM0006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 KW Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 650
 FT DOMAIN 22 580
 FT TRANSMEM 581 603
 FT DOMAIN 604 650
 FT DOMAIN 640 643
 FT DOMAIN 241 247
 FT DOMAIN 264 268
 FT CARBOHYD 337 337
 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 551 551 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 48 48 P -> A (IN REF. 2).
 SQ SEQUENCE 650 AA: 72202 MW: 121A034B708C67CA CRC64;

Query Match 28.5%; Score 1150.5; DB 1; Length 650;
 Best Local Similarity 35.7%; Pred. No. 2,6e-53;
 Matches 279; Conservative 114; Mismatches 218; Indels 171; Gaps 20;

OY 1 MRLGALLL-----LAAMTARALEVDTGDNAGLAEPOQAMFCGRILNMHNMNQNGKW 52
 DB 23 LRLPLLLRLRAQPAIGSLAGSGSPGAPAP-6SA-----QVAGLCGRLLTRDLRTGRW 74
 OY 53 DSDPSGKTCTDKEGSILOVCEVYPELOITNVANOPVTIONCKGRKCKTHPHF- 111
 DB 75 EBDPGRRCRLCDPQVLEYCKQMPPELOIARVEDATQAIPIHRRNGGSRSSCAHPHQ 134
 OY 112 VTPYCLGVEYSDALVPDKCKFLHOERMDVCEFHLMHMYAKETCEKSTNLHDYGM 171
 DB 135 VVPEFCLGEEFSEALVPEGCRFLHOERMDQESSTRHQAORACSSOGILHSGML 194
 OY 172 LPCGIDKRGVFEVCCPLAEESDNDVSDAEEDSDVMWGADTDYADGSEKVVAEAE 231
 DB 195 LPCGDRRGVEYVCCPPPTPD--PSTANGDPSTRSW-----PESGR--VEGAE 242
 OY 232 EVAAVEEEDADDDEDEDEDEVEEAEPEYBEATERTTSIATTTTTTTEVEEVREV 291
 DB 243 EE-----EESFPQVDDYFVEVPPQAEDEE----- 267
 OY 292 SEQATGPGRAMISRWYEDVTEGKCAPFFYGGCGGNRRNNTDEYKQMAVCGSAMSOLIK 351
 DB 268 -----ETVP-----DGVITFGMPGEISEHGEFLAKMDLERRRRQINEVNR 283
 OY 352 TQGEPLANDPVKLPPTAASPDAVDKYLETPGDENENHAFOKAKERLEAKHEMSOYVR 411
 DB 284 VT-----PIPRPT-----DGVITFGMPGEISEHGEFLAKMDLERRRRQINEVNR 330
 OY 412 EWEAEARQAKNLPRKADKRAVIOHFOEKVESLROEANERQOLVETHMAVEMALNDRL 471
 DB 331 EWAMADNOSKNLPKADROLNENHPOSIIQTELEOYSGEORLVEHATRYVALINDORA 390
 OY 472 ALENTITALOAVPRPRHVENMLKRYRAEOKROHTLKHFEHVRVDPKKAQIRSOVM 531
 DB 391 ALEGLLAQADPPQAEERVLRLRYLRAEKEORHTLKHGYHVAADPEKQOQRVYH 450
 OY 532 THLRVYERBNOSTSLVNVPAVAEIODEVDELLOKEVNDVLANNISPRISYGN 591
 DB 451 THLOYIEERVNOSTLGLDONPHLAOELRPQIOELHSEH----- 489
 OY 592 ALMPSLTETKTVELLPVNGEFLD--DLQPHSFGADSVAPANTENEVEPYDARPADRG 649
 DB 490 -LGPSELEA-----PAPGSSSEDKGGLQPRDS--KDDTPH-----TLRKG 526
 OY 650 LTRRGSGITNKITEIESEVKMADEFRIHDSGYEVH--OKLVEFAEDVSKKAIIGLM 706
 DB 527 STEODAAPSEKEMPLDQYERKNAVASVPRPFSSSEIORDDELAPAGGVSAEASGL 586
 OY 707 VGVVIAIVIVITLVM--KKKOYTSIHGVYVDAVTPPEERHLKMOONGENETPKYKF 765
 DB 587 IMGAGGSLIYISKLLRKKRYGAIISGVYEVDPMLTEEQLEKLODHGENTPTYRFL 646
 OY 766 EQ 767
 DB 647 EE 648

RESULT 9
 APPL_MOUSE STANDARD: PRT: 653 AA.
 ID APPL_MOUSE AC 003157;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE Amyloid-like protein 1 precursor (APLP).
 GN APLP.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93066322; PubMed=1279693;
 RA Masco W., Bupp K., Magendantz M., Gussella J.F., Tanzi R.E.,
 RA Solomon F.;
 RT "Identification of a mouse brain cDNA that encodes a protein related
 to the Alzheimer disease-associated amyloid beta protein precursor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. MAY BE PROCESSED
 IN THE GOLGI COMPLEX; HOWEVER, IT IS NOT YET CLEAR WHETHER APLP
 IS SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: L04538; AAA37247.1; -;
 DR PIR: A46362; A46362.
 DR HSSP: P05067; IMPV.
 DR MCD: MGI:88046; APLP1.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM0006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 KW Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 653
 FT DOMAIN 21 583
 FT TRANSMEM 584 606
 FT DOMAIN 607 653
 FT DOMAIN 643 646
 FT DOMAIN 263 271
 FT DOMAIN 464 464
 FT CARBOHYD 464 554
 FT CARBOHYD 554 554
 SQ SEQUENCE 653 AA: 72751 MW: 56516DC3EA40E4B0 CRC64;
 Query Match 28.4%; Score 1150.5; DB 1; Length 653;
 Best Local Similarity 35.4%; Pred. No. 4,8e-53;
 Matches 274; Conservative 120; Mismatches 228; Indels 153; Gaps 19;

OY 1 MRLGALLLAAWTARA-LEVPTDGNAGLAEPOQAMFCGRILNMHNMNQNGKWDSPSGT 59
 DB 22 LRLPLLLRLRAQPAIGSLAGSGSPGAPAP-6SA-----QVAGLCGRLLTRDLRTGRW 74
 OY 60 KTCIDTKFKGILOVCEVYPELOITNVANOPVTIONCKGRKCKTHPHF-VTPYCL 118
 DB 81 RCLLDQVLEYCKQMPPELOIARVEDATQAIPIHRRNGGSRSSCAHPHQ 134
 OY 112 VTPYCLGVEYSDALVPDKCKFLHOERMDVCEFHLMHMYAKETCEKSTNLHDYGM 178
 DB 135 VVPEFCLGEEFSEALVPEGCRFLHOERMDQESSTRHQAORACSSOGILHSGMLPCGSDR 200
 OY 172 LPCGIDKRGVFEVCCPLAEESDNDVSDAEEDSDVMWGADTDYADGSEKVVAEAEV 237
 DB 195 LPCGDRRGVEYVCCPPPTPD--PSTANGDPSTRSW-----PESGR--VEGAE 248
 OY 232 EVAAVEEEDADDDEDEDEDEVEEAEPEYBEATERTTSIATTTTTTTEVEEVREV 297
 DB 243 EE-----EESFPQVDDYFVEVPPQAEDEE----- 281

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QY 298 GPCRAMISRWYEDVTEGCAAPFYGGCGGNRNNDTEECYCAVCSAMSQSLKTTQEP 357
D 282 ---WVSR-----VT----- 288
OY 358 ARDPVKLPTTAASTDPAVDKYLETPGDENEHAFQAKERLEAKHERMSQVREWEAE 417
D 289 ---PVPRT-----DGYDVFGEFGEIGEHGFLRAKMDLERMROINEVREMAAD 339
QY 418 ROAKNIIPRAKKAVIOHFEKEVESLEOEAANERQOLVETHMARVAMINDRRALALENYI 477
D 340 SSKRLPKRADQALNEHQSLIQTLEREGYSGRGVLVETHTATVIALINDORRALDEGFL 399
OY 478 TALQAVPRPRHRYEMMLKKYVAEOKROHITLKEHYRANVDPKAAQIRSOVTHLRYI 537
D 400 AALQDPPOAEVYLMALRYLAKEOEKORHTLRHYOHAADVPEKAOQMRFOVQTHLQVI 459
OY 538 YERNMOSLSLLYNPAVAEIOEDVELLOKQNSDVLNMMISEPRISGNDALAM-S 596
D 460 EERNMOSLGLDQNDHLOELPQLOELL-----LAHLLPSEL---DASVPGS 505
OY 597 LLETKTVELLPVNGEFSLDLOPWHSGADSVPAANTEVEPVDPARPAADGLTTRPGS 656
D 506 SSEOK-----GSLQ-----PESKDDPYTLT---KGTIDQESS 536
OY 657 GLTNKTEISEVKMDAEFRHDSGYEVNH---QKLVFAEDVGSKKAIGILMVGCVIA 713
D 537 SSGREKLPPLDEQYEQKVNASAPRCFPFHSIDQDELAPSGTGVAREALSGILLINGAGG 596
OY 714 TVIVTTLML-KKKQYTSIHGVYVDAVAPPEERHLSKMOONGENPTPKFEQ 767
D 597 SLIVSLLLKRRKPYGTISHGVYVDAVAPPEERHLSKMOONGENPTPKFEQ 651

```

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RESULT 10
A4 DROME ID STANDARD: PRT: 886 AA.
AC P14599:
D 01-APR-1990 (Rel. 14, Created)
D 01-APR-1990 (Rel. 14, Last sequence update)
D 16-OCT-2001 (Rel. 40, Last annotation update)
D Beta-amyloid-like protein precursor.
D DE APPL OR VND.
O Drosophila melanogaster (Fruit fly).
O Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
O Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
O Ephydroidea; Drosophilidae; Drosophila.
O NCBI_Taxid=7227;
D 11
D SEQUENCE FROM N.A.
D MEDLINE=89184650; PubMed=2494667;
D Rosen D.R., Martin-Morris L., Luo L., White K.;
D "A Drosophila gene encoding a protein resembling the human
D beta-amyloid protein precursor.";
D Proc. Natl. Acad. Sci. U.S.A. 86:2478-2482(1989).
D 12
D SEQUENCE OF 1-83 FROM N.A.
D MEDLINE=91184006; PubMed=2127912;
D Martin-Morris L.E., White K.;
D "The Drosophila transcript encoded by the beta-amyloid protein
D precursor-like gene is restricted to the nervous system.";
D Development 110:185-195(1990).
D 13
D FUNCTION: PROBABLY CORRESPONDS TO THE PROTEIN ENCODED BY THE
D ESSENTIAL LOCUS VND, A GENE REQUIRED FOR EMBRYONIC NERVOUS
D SYSTEM DEVELOPMENT.
D 14
D SUBCELLULAR LOCATION: Type I membrane protein.
D 15
D TISSUE SPECIFICITY: APPL TRANSCRIPTS ARE FOUND IN THE CENTRAL AND
D PERIPHERAL NERVOUS SYSTEMS. WITHIN THE NERVOUS SYSTEM TRANSCRIPTS
D ARE NOT OBSERVED IN NEUROBLASTS, NEWLY GENERATED NEURONS AND AT
D LEAST ONE CLASS OF PRESUMED GLIAL CELLS.
D 16
D DEVELOPMENTAL STAGE: APPL TRANSCRIPTS ARE FOUND IN POST-MITOTIC
D NEURONS IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS IN ALL
D DEVELOPMENTAL STAGES.

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CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
D EMBL: J04516; AAA28874.1; -
D EMBL: X55774; CA339294.1; -
D EMBL: X55775; CA339294.1; JOINED.
D PIR: A32758; A32758.
D HSSP: P05067; IMMP.
D FlyBase: FBgn000108; Appl.
D InterPro: IPR001868; A4_APP.
D Pfam: PF02177; A4_EXTRA; 1.
D SMART: SM00006; A4_EXTRA; 1.
D PROSITE: PS00319; A4_EXTRA; 1.
D PROSITE: PS00320; A4_INTA; 1.
D Signal: Transmembrane; Amyloid; Neurogenesis.
D SIGNAL: 1 27
D CHAIN: 28 886
D DOMAIN: 28 810
D TRANS: 811 833
D DOMAIN: 834 886
D CARBOHYD: 150 150
D CARBOHYD: 161 161
D CARBOHYD: 236 236
D CARBOHYD: 239 239
D CARBOHYD: 573 573
D SEQUENCE: 886 AA; 98261 MW; C51EA4194D5A8D CRC64;
Query Match 18.2%; Score 737.5; DB 1; Length 886;
Best Local Similarity 24.7%; Pred. No. 2.2e-31;
Matches 235; Conservative 137; Mismatches 313; Indels 265; Gaps 30;
OY 7 LLLLAAMTARALEVPTDNCAGLA-----EPOIAMFC--GRIMHMNV--QNGKMDSPSG 58
D 9 LLLRSWVYLA-----GTAQVQASPRMPEQIANVLCAGQIYQYQYLSSEBRWYTDLSK 63
OY 59 T---KTCTIDKEGILQYCOEYVPELOITNVVYANQVPTIQNCKRG---RQCKTHPHV 112
D 64 KTTGCTCLRDMDLIDYCKKAYPNRDNIVYESSHYOKIGGCRGALNAACKSGSHWI 123
OY 113 IYRCLVEFVSDALLVYDCKFLQERMDYCETLHMHYAKETCSKSTYLHXYGML 172
D 124 KPFRL-GPFOSDALLVPEGCLFDHINASRCWPFVRNQTGAACQOERGMQRTFAML 182
OY 173 PCGIDKFRGVFFVCCP-----LAEESDNDV---SA 199
D 183 PCGISVFGVFEVCCPKFKTDEIHVKTTDLPVMPAQAINGANDELMNDEDDSDNSNYSK 242
OY 200 DAEDSDVMMGADTDYADGSEDKVVEAEVEEY-----AEV 237
D 243 DANEDDL-----DEDLMDDDEEDMDVADAEATAGSGSPWTSSGSDNSGLDINAEY 296
OY 238 EE-EEADDEDDDEDDGDEVEEAEVEEYEA-TERTSITATTTTTSVEEYVREVCSDA 295
D 297 DSGEGDNYEEDGAGSEAEVEASWDSGAKVYSLKSDSSPSAPAVAPAPKAPYKS 356
OY 296 ETGFCRAMISRWDVTEGKCAAPFYGGCGGNRNNDTEECYCAVCSAMSQSLKTTQEP 355
D 357 ESVSTPQLS-----ASAAAFVYANSNSGT-----GAGAPRSTQPTSD 396
OY 356 PLADPVKLPPTTAASTDPAVDKYLETPGDENEHAFQAKERLEAKHERMSQVREWEAE 415
D 397 P-----YTHFDPRHYEQHSYKVSQKRLSEHREKVTYRVAKMDSD 435
OY 416 AERQAKNLPKADKA-----VIQHOKEKVESLEOEAANERQOLVETHMARVAMINDR 468

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Db 436 LEEKYDMLADPKAAQSEKQMTARFOTSVQALEEGNAEKHQLAMHQVLAHINOR 495
 QY 469 RLTALENTITALQAVPPRRPHVNNLKKYVRAEOKDRQHTLKHFEH-VRMVP---KRAA 524
 Db 466 KREANTCTTQALTEOPPPNNAHVEKCLQKLRALKDRALAHNHLNLSGGSGGLEAA 555
 QY 555 QIRSQVMTHLYRYERMQSLSLYNVPAVAEEI-----ODEV-----562
 Db 556 SERPPTLELIDRAVQNSMTLKRYPLESAKINQIMNDYILALRSDDIGSSLSGME 615
 QY 563 -----DELLOEQNYSDDVLAN 579
 Db 616 EAEGILDKRYVEIERKVAEKERLRLAEQKQRAERERLEKRLKLEAKVMDLKS 675
 QY 580 MISE-----PRISYNDALM-----PSLTETKTVELLPNG 611
 Db 676 QVAEQSQPTQSSQSQAOQQQEKSLPEKELGPDALVTANPULETKS-----726
 QY 612 EFSLDDLPWHSFGADSPVANTENEVEPDARPAADRCGLTPRSGSLNIKTEISEYKM 671
 QY 727 EKDSLDT-----YGEATVSTTKVQTVLPTVDDAVQRAVEDVAA-----VAHQEA 773
 QY 672 DAEFHDHSGYEYHOKLYF-----FAEDVGSNK---GAILGLMGGVVIATVITLVM 723
 Db 774 EPOVQHFMTHDIGHRESEFSLRFEFAQHAHAKEGRNRYFTLSFGAILMAAFVGVAVA 833
 QY 724 KKKQYTSIH-HGVVEVDAAVTP-----EERLSKMQONGYENPYKFE 766
 Db 834 KWRSRSRPHAQGFIEVDONVTTHPIVREKIVPMQINGENPYKYFE 883

RESULT 11

A4_MACEFA STANDARD: PRT: 87 AA.
 ID A4_MACEFA

AC P53601;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein (Fragment).
 GN APP.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Macaca.
 CX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL MEDLINE=9127311; PubMed=1905108;
 RT Podlasy M.B., Tolan D.R., Selkoe D.J.;
 RT "Homology of the amyloid beta protein precursor in monkey and human
 RT supports a primate model for beta amyloidosis in Alzheimer's
 RT disease".
 RL Am. J. Pathol. 138:1423-1435(1991).
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC
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 CC
 CC EMBL: M58726; AAA36828.1; -.
 CC PIR: S06678; 1AAP.
 CC HSSP: P05067; 1AAP.

DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI.1.
 DR PRINTS: PR00759; BASICPTASE.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4-EXTRA; PARTIAL.
 DR PROSITE: PS00320; A4-INTRA; PARTIAL.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Alternative splicing;
 KM Serine protease inhibitor.
 FT NON_TER 1
 FT DOMAIN 4 79 BPTI/KUNITZ INHIBITOR.
 FT ACT_SITE 16 17 REACTIVE BOND.
 FT DISULFID 6 56 BY SIMILARITY.
 FT DISULFID 15 39 BY SIMILARITY.
 FT DISULFID 31 52 BY SIMILARITY.
 FT NON_TER 87
 SQ SEQUENCE 87 AA: 9608 MW: 676690DEDEE7FF CRC64;
 Query Match 11.38; Score 457; DB 1; Length 87;
 Best Local Similarity 95.48; Pred. No. 5,1e-18;
 Matches 83; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 286 VREVCSQATGPGCRAMISRMVFDTEGKCAPFYGGCGGGRNNRNPDEEYCMAYCSAM 345
 Db 1 VREVCSQATGPGCRAMISRMVFDTEGKCAPFYGGCGGGRNNRNPDEEYCMAYCSAM 60
 QY 346 SSSLKTKTQEPRLARDPVKLPPTAASP 372
 Db 61 SSSLKTKTREPRLRDVPVKLPPTAASP 87

RESULT 12

A4_MACMU STANDARD: PRT: 76 AA.
 ID A4_MACMU

AC P29216;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein (Fragment).
 GN APP.
 OS Macaca mulatta (Rhesus macaque).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Macaca.
 CX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL TISSUE-Brain.
 RA Koo E.H., Sisodia S.S., Price D.L.;
 RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC
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 CC
 CC EMBL: X15985; CAA34116.1; -.
 CC PIR: S06678; S06678.
 CC HSSP: P05067; 1TAW.

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DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4-EXTRA; PARTIAL.
DR PROSITE: PS00320; A4-INTRA; PARTIAL.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR Glycoprotein: Amyloid; Neurone; Alternative splicing;
KW Serine protease inhibitor.
FT NON_TER 1 1
FT DOMAIN 1 76 BPTI/KUNITZ INHIBITOR.
FT ACET SITE 13 14 REACTIVE BOND.
FT DISULFID 3 53 BY SIMILARITY.
FT DISULFID 12 36 BY SIMILARITY.
FT DISULFID 28 49 BY SIMILARITY.
FT NON_TER 76 76
SQ SEQUENCE 76 AA; 8527 MW; 492BF3069AB082A1 CRC64;

Query Match 9.9%; Score 403; DB 1; Length 76;
Best Local Similarity 94.7%; Pred. No. 2.8e-15;
Matches 72; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 289 EVCSEQAEATGCPGRAMISRYFDYTEGKCAPFFYGGCGGNRNFDREYCMAYCGSAMSSQ 348
DB 1 EVCSQAEATGCPGRAMISRYFDYTEGKCAPFFYGGCGGNRNFDREYCMAYCGSAMSSQ 60
QY 349 LKKTQEPPLADPKVL 364
DB 61 LKKTREPPLRDPKVL 76

RESULT 13
A4_BOVIN STANDARD; PRT; 59 AA.
ID A4_BOVIN
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-Ap4) (A-beta)] (Fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A.
Tissue-Brain:
MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305 (1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X56124; CAA39589.1; -
DR EMBL: X56126; CAA39591.1; -
DR HSSP: P05067; 1BA4.

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DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4-EXTRA; PARTIAL.
DR PROSITE: PS00320; A4-INTRA; PARTIAL.
KW Glycoprotein: Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 7.2%; Score 292; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 666 ISEVKMDAEFRHDSGYEVHHOKLVFFADVGSNKAIGILMGVAVITVITLMLK 724
DB 1 ISEVKMDAEFRHDSGYEVHHOKLVFFADVGSNKAIGILMGVAVITVITLMLK 59

RESULT 14
A4_RABIT STANDARD; PRT; 58 AA.
ID A4_RABIT
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-Ap4) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
[1]
SEQUENCE FROM N.A.
Tissue-Brain:
MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305 (1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
DR EMBL: X56129; CAA39594.1; -
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4-EXTRA; PARTIAL.
DR PROSITE: PS00320; A4-INTRA; PARTIAL.
KW Glycoprotein: Amyloid; Neurone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 7.1%; Score 288; DB 1; Length 58;

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Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 667 SEVKMDAEFRHDSGYEVHOKLVEFAEDVGSNKGAIIGLMGCVVIATVITVITLMK 724
DB 1 SEVKMDAEFRHDSGYEVHOKLVEFAEDVGSNKGAIIGLMGCVVIATVITVITLMK 58

RESULT 15

A4_SHEEP STANDARD: PRT: 58 AA.

AC Q28737;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-A4p) (A-beta)] (Fragment).
GN APP.

OS Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.

OX NCBI_TaxID=9940;

RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

RX MEDLINE=92017079; PubMed=1656157;

RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

"Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species

RT polymerase chain reaction analysis.";

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

-1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

G/O) (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: Type I membrane protein.

-1- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL: X56130; CAA39595.1; -

DR HSP; P05067; IAML.

DR InterPro: IPR001868; A4_APP.

DR PROSITE: PS00319; A4_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4_INTRA; PARTIAL.

KM Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 1

FT CHAIN 6 48

FT DOMAIN <1 33

FT TRANSMEM 34 57

FT DOMAIN 58 >58

FT NON_TER 58 58

FT SEQUENCE 58 AA: 6300 MW: F434209D88EBA82D CRC64;

FT CYTOPLASMIC (POTENTIAL).

FT EXTRACELLULAR (POTENTIAL).

FT POTENTIAL.

FT CYTOPLASMIC (POTENTIAL).

FT POTENTIAL.

FT CYTOPLASMIC (POTENTIAL).

FT POTENTIAL.

FT CYTOPLASMIC (POTENTIAL).

FT POTENTIAL.

FT CYTOPLASMIC (POTENTIAL).

FT POTENTIAL.

FT CYTOPLASMIC (POTENTIAL).

FT POTENTIAL.

FT CYTOPLASMIC (POTENTIAL).

FT POTENTIAL.

FT CYTOPLASMIC (POTENTIAL).

Search completed: October 31, 2002, 10:12:24
Job time : 21.048 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:56 ; Search time 1.16359 Seconds
(without alignments)
902.637 Million cell updates/sec

Title: US-09-785-215-2_COPY_672_714

Perfect score: 222
Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....VGSNKGAIIGLMVGVVIAT 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/Backfilest1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	222	100.0	43 1 US-08-235-400-1	Sequence 1, Appli
2	222	100.0	43 1 US-08-437-067-1	Sequence 1, Appli
3	222	100.0	43 1 US-08-302-808-6	Sequence 6, Appli
4	222	100.0	43 1 US-08-079-511-1	Sequence 1, Appli
5	222	100.0	43 1 US-08-467-607-1	Sequence 1, Appli
6	222	100.0	43 2 US-08-404-831-1	Sequence 1, Appli
7	222	100.0	43 2 US-08-602-264A-3	Sequence 3, Appli
8	222	100.0	43 2 US-08-469-362-1	Sequence 1, Appli
9	222	100.0	43 2 US-08-612-785B-1	Sequence 1, Appli
10	222	100.0	43 2 US-08-475-579A-1	Sequence 1, Appli
11	222	100.0	43 2 US-08-850-392-1	Sequence 1, Appli
12	222	100.0	43 2 US-08-986-948-6	Sequence 6, Appli
13	222	100.0	43 2 US-08-975-977-1	Sequence 1, Appli
14	222	100.0	43 2 US-08-817-423-1	Sequence 1, Appli
15	222	100.0	43 2 US-08-920-162A-1	Sequence 1, Appli
16	222	100.0	43 3 US-08-461-018A-3	Sequence 3, Appli
17	222	100.0	43 3 US-08-976-191-1	Sequence 1, Appli
18	222	100.0	43 3 US-08-976-179-1	Sequence 1, Appli
19	222	100.0	43 4 US-09-216-958-3	Sequence 3, Appli
20	222	100.0	43 4 US-09-356-931-1	Sequence 1, Appli
21	222	100.0	43 4 US-08-733-202-1	Sequence 1, Appli
22	222	100.0	43 4 US-08-703-675C-1	Sequence 1, Appli
23	222	100.0	43 4 US-09-390-692-1	Sequence 1, Appli
24	222	100.0	43 4 US-08-617-267C-1	Sequence 1, Appli
25	222	100.0	43 4 US-09-303-655-1	Sequence 1, Appli
26	222	100.0	47 2 US-08-609-090-10	Sequence 10, Appli
27	222	100.0	52 2 US-08-609-090-11	Sequence 11, Appli

28	222	100.0	53 4 US-09-173-887-5	Sequence 5, Appli
29	222	100.0	59 1 US-08-484-969-3	Sequence 3, Appli
30	222	100.0	59 1 US-08-472-627-3	Sequence 3, Appli
31	222	100.0	59 1 US-08-388-463-3	Sequence 3, Appli
32	222	100.0	63 1 US-08-462-859A-4	Sequence 4, Appli
33	222	100.0	63 1 US-08-123-659A-4	Sequence 4, Appli
34	222	100.0	63 1 US-08-464-247A-4	Sequence 4, Appli
35	222	100.0	63 1 US-08-464-248A-4	Sequence 4, Appli
36	222	100.0	99 2 US-08-422-333-3	Sequence 3, Appli
37	222	100.0	99 3 US-08-339-708A-8	Sequence 4, Appli
38	222	100.0	99 3 US-08-339-708A-8	Sequence 8, Appli
39	222	100.0	100 6 5187153-10	Patent No. 5187153
40	222	100.0	100 6 5220013-10	Patent No. 5220013
41	222	100.0	100 6 5223482-10	Patent No. 5223482
42	222	100.0	103 2 US-08-404-831-2	Sequence 2, Appli
43	222	100.0	103 2 US-08-612-785B-2	Sequence 2, Appli
44	222	100.0	103 2 US-08-475-579A-2	Sequence 2, Appli
45	222	100.0	103 2 US-08-920-162A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-235-400-1
Sequence 1, Application US/08235400
Patent No. 5552426
GENERAL INFORMATION:
APPLICANT: Lunn, William H.
APPLICANT: Monn, James A.
TITLE OF INVENTION: METHODS FOR TREATING A PHYSIOLOGICAL
TITLE OF INVENTION: DISORDER ASSOCIATED WITH BETA AMYLOID PEPTIDE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/1104
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/235.400
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36, 808
REFERENCE/DOCKET NUMBER: X-9507
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-235-400-1

Query Match 100.0% Score 222: DB 1: Length 43;
Best Local Similarity 100.0% Pred. No. 3.2e-27;
Matches 43: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 DAEFRHDSGYEVHHQKLVFFADVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHQKLVFFADVGSNKGAIIGLMVGVVIAT 43

RESULT 2

US-08-437-067-1

Sequence 1, Application US/08437067
Patent No. 5593846

GENERAL INFORMATION:

APPLICANT: Schenk, Dale B.
APPLICANT: Selkoe, Dennis J.
APPLICANT: Schlossmacher, Michael G.
APPLICANT: Seubert, Peter A.

APPLICANT: Vingo-Pellfrey, Carmen

TITLE OF INVENTION: Methods and Compositions for
Detection
TITLE OF INVENTION: of Soluble Beta-Amyloid Peptide

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend

STREET: One Market Plaza, Stewart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/437,067

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/965,972

FILING DATE: 26-OCT-1992

APPLICATION NUMBER: US 07/911,647

FILING DATE: 10-JUL-1992

ATTORNEY/AGENT INFORMATION:

NAME: Heslin, James M.

REGISTRATION NUMBER: 29,541

REFERENCE/DOCKET NUMBER: 15270-6-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 43 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-437-067-1

Query Match

Best Local Similarity 100.0%; Score 222; DB 1; Length 43;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVNHOKLVFAEDVGSNKGAIITGLMVGCVIAT 43

Db 1 DAEFRHDSGYEVNHOKLVFAEDVGSNKGAIITGLMVGCVIAT 43

RESULT 3

US-08-302-808-6

Sequence 6, Application US/08302808

Patent No. 5750349

GENERAL INFORMATION:

APPLICANT: Suzuki, No. 5750349uh1ro

APPLICANT: ODAKA, Asano

APPLICANT: KITADA, Chieko

TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR

DERIVATIVES AND USE THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

STREET: 130 WATER STREET

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02019

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/302,808

FILING DATE: 15-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP94/00089

FILING DATE: 24-JAN-1994

APPLICATION NUMBER: 010132/1993

FILING DATE: 25-JAN-1993

APPLICATION NUMBER: 019035/1993

FILING DATE: 05-FEB-1993

APPLICATION NUMBER: 286985/1993

FILING DATE: 16-NOV-1993

APPLICATION NUMBER: 334773/1993

FILING DATE: 28-DEC-1993

ATTORNEY/AGENT INFORMATION:

NAME: DAVID, RESNICK S

REGISTRATION NUMBER: 34,235

REFERENCE/DOCKET NUMBER: 44631

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 43 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

US-08-302-808-6

Query Match

Best Local Similarity 100.0%; Score 222; DB 1; Length 43;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVNHOKLVFAEDVGSNKGAIITGLMVGCVIAT 43

Db 1 DAEFRHDSGYEVNHOKLVFAEDVGSNKGAIITGLMVGCVIAT 43

RESULT 4

US-08-079-511-1

Sequence 1, Application US/08079511

Patent No. 5766846

GENERAL INFORMATION:

APPLICANT: Schenk, Dale B.

APPLICANT: Selkoe, Dennis J.

APPLICANT: Schlossmacher, Michael G.

APPLICANT: Seubert, Peter A.

APPLICANT: Vingo-Pellfrey, Carmen

TITLE OF INVENTION: Methods and Compositions for Detection

TITLE OF INVENTION: of Soluble Beta-Amyloid Peptide

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend

STREET: One Market Plaza, Stewart Tower, Suite 2000

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/079,511
FILING DATE: 19930617
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,972
FILING DATE: 26-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-6-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-079-511-1

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERHDSGYEVHHOKLVEFAEDVGSNKGATIGLMVGSVIAT 43
DB 1 DAERHDSGYEVHHOKLVEFAEDVGSNKGATIGLMVGSVIAT 43

RESULT 5
US-08-467-607-1
Sequence 1, Application US/08467607
Patent No. 5783434
GENERAL INFORMATION:
APPLICANT: TUNG, JAY S.
APPLICANT: SINHA, SUKANTO
APPLICANT: MCCONLOGUE, LISA
APPLICANT: TRISUNO, GWEN
APPLICANT: ANDERSON, JOHN
APPLICANT: CHRYSLER, SUSANNA
TITLE OF INVENTION: NOVEL CATEPSIN AND METHODS AND
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHENA NEUROSCIENCES
STREET: 800 F. Gateway Blvd.
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,607
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DUVALL, JEAN M.

REGISTRATION NUMBER: 32,731
REFERENCE/DOCKET NUMBER: 002010-007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-8370
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-607-1

Query Match 100.0%; Score 222; DB 1; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERHDSGYEVHHOKLVEFAEDVGSNKGATIGLMVGSVIAT 43
DB 1 DAERHDSGYEVHHOKLVEFAEDVGSNKGATIGLMVGSVIAT 43

RESULT 6
US-08-404-831-1
Sequence 1, Application US/08404831
Patent No. 5817626
GENERAL INFORMATION:
APPLICANT: Mark A. Findels, Howard Benjamin, Marc B. Garnick,
APPLICANT: Malcolm L. Gelfer, Arvind Hundal, Laura Kasman,
APPLICANT: Gary Musso, Ethan R. Signer, and James Wakefield
TITLE OF INVENTION: Modulators of [SYMBOL 98 \f "Symbol"]-Amyloid Peptide Aggre
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/404,831
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hanley, Elizabeth A. (EAH)
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: PPI-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-404-831-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERHDSGYEVHHOKLVEFAEDVGSNKGATIGLMVGSVIAT 43
DB 1 DAERHDSGYEVHHOKLVEFAEDVGSNKGATIGLMVGSVIAT 43

Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 7

US-08-602-264A-3
Sequence 3, Application US/08602264A
Patent No. 5837853

GENERAL INFORMATION:

APPLICANT: AKIHKO TAKASHIMA et al.

TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR

TITLE OF INVENTION: ALZHEIMER'S DISEASE, A SCREENING METHOD OF ALZHEIMER'S DISEASE

TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

COUNTRY: D.C.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch,

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/602,264A

FILING DATE: February 20, 1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/204,091

FILING DATE: March 2, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE:

TELEFAX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 43 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-602-264A-3

Query Match 100.0%; Score 222; DB 2; Length 43;

Best Local Similarity 100.0%; Pred. No. 3,2e-27;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 8

US-08-469-362-1
Sequence 1, Application US/08469362
Patent No. 5849711

GENERAL INFORMATION:

APPLICANT: TUNG, JAY S.

APPLICANT: SINHA, SUKANTO

APPLICANT: MCCONLOGUE, LISA

TITLE OF INVENTION: SEMKO, CHRISTOPHER M.F.

TITLE OF INVENTION: NOVEL CATEPSIN AND METHODS AND

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: ATHENA NEUROSCIENCES

STREET: 800 F. Gateway Blvd.

CITY: South San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,362

FILING DATE: 06-JUN-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: DUVAL, JEAN M.

REGISTRATION NUMBER: 32,731

REFERENCE/DOCKET NUMBER: 002010-005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 877-0900

TELEFAX: (415) 877-8370

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 43 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-469-362-1

Query Match 100.0%; Score 222; DB 2; Length 43;

Best Local Similarity 100.0%; Pred. No. 3,2e-27;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGSVIAT 43

RESULT 9

US-08-612-785B-1
Sequence 1, Application US/08612785B
Patent No. 5854204

GENERAL INFORMATION:

APPLICANT: Findels, Mark A. et al.

TITLE OF INVENTION: Ab peptides that modulate b-Amyloid

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 28 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109-1875

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/612,785B

FILING DATE: Herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/404,831

FILING DATE: 14-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/475,579

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/548,998

FILING DATE: 27-OCT-1995

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A.

REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-785B-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATIGLWGGVVIAT 43
1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATIGLWGGVVIAT 43

RESULT 10
US-08-475-579A-1
Sequence 1, Application US/08475579A
Patent No. 5854215
GENERAL INFORMATION:
APPLICANT: Mark A. Flindeis et al.
TITLE OF INVENTION: Modulators of (SYMBOL 98 \f "Symbol")-Amyloid Peptide Aggrega
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,579A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/404,831
FILING DATE: 14-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: P41,106
REFERENCE/DOCKET NUMBER: PPI-002CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-475-579A-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATIGLWGGVVIAT 43
1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATIGLWGGVVIAT 43

Db 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATIGLWGGVVIAT 43

RESULT 11
US-08-850-392-1
Sequence 1, Application US/08850392
Patent No. 5858982
GENERAL INFORMATION:
APPLICANT: TUNG, JAY S.
APPLICANT: SINHA, SUKANTO
APPLICANT: MCCONLOGUE, LISA
APPLICANT: SEMKO, CHRISTOPHER M.F.
TITLE OF INVENTION: NOVEL CATEPSIN AND METHODS AND
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: ATHENA NEUROSCIENCES
STREET: 800 F. Gateway Blvd.
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,392
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,362
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: DUVAL, JEAN M.
REGISTRATION NUMBER: 32,731
REFERENCE/DOCKET NUMBER: 002010-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 877-0900
TELEFAX: (415) 877-8370
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-850-392-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATIGLWGGVVIAT 43
1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATIGLWGGVVIAT 43

RESULT 12
US-08-986-948-6
Sequence 6, Application US/08986948
Patent No. 595317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 595317uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON

STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
STRANDEDNESS: single
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-6

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAFFRHDSGYEVHHOKLVFFAEDVGSNKGATITGLMVGCVIAT 43
DB 1 DAFFRHDSGYEVHHOKLVFFAEDVGSNKGATITGLMVGCVIAT 43

RESULT 13
US-08-975-977-1
Sequence 1, Application US/08975977
Patent No. 5965614
GENERAL INFORMATION:
APPLICANT: JAMES E. AUDIA
APPLICANT: BEVERLY K. FOLMER
APPLICANT: VARGHESE JOHN
APPLICANT: LEE H. LATIMER
APPLICANT: JEFFREY S. NISSEN
APPLICANT: JON K. REEL
APPLICANT: EUGENE D. THORSETT
APPLICANT: CELIA A. WHITESITT
TITLE OF INVENTION: N-(ARYL/HEPTEROARYL) AMINO
TITLE OF INVENTION: ACID ESTERS, PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS COMPRISING SAME, AND
TITLE OF INVENTION: METHODS FOR INHIBITING BETA-AMYLOID
TITLE OF INVENTION: PEPTIDE RELEASE AND/OR ITS

TITLE OF INVENTION: SYNTHESIS BY USE OF SUCH COMPOUNDS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker &
ADDRESSEE: Mathis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,977
FILING DATE: Unassigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/755,444
FILING DATE: 22 NO. 5965614ember 1996
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 002010-044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-854-7400
TELEFAX: 650-854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-975-977-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAFFRHDSGYEVHHOKLVFFAEDVGSNKGATITGLMVGCVIAT 43
DB 1 DAFFRHDSGYEVHHOKLVFFAEDVGSNKGATITGLMVGCVIAT 43

RESULT 14
US-08-617-423-1
Sequence 1, Application US/08617423
Patent No. 5972634
GENERAL INFORMATION:
APPLICANT: TANZI, RUDOLPH E.
APPLICANT: BUSH, ASHLEY I.
APPLICANT: MOIR, ROBERT D.
TITLE OF INVENTION: A Diagnostic Assay for Alzheimer's
TITLE OF INVENTION: Disease: Assessment Of A Abnormalities
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,423
FILING DATE: 4-AUG-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US94/11895
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 0609.4110000/REF/JUK
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-817-423-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAFFRHDSGYEVHHQKLVFAEDVGSNKGALITGLMVGCVIAT 43
DB 1 DAFFRHDSGYEVHHQKLVFAEDVGSNKGALITGLMVGCVIAT 43

RESULT 15
US-08-920-162A-1
Sequence 1, Application US/08920162A
Patent No. 5985242
GENERAL INFORMATION:
APPLICANT: Findeis, M. et al.
TITLE OF INVENTION: Modulators of (SYMBOL 98 \f "Symbol")-Amyloid Peptide
TITLE OF INVENTION: Aggregation Comprising D-Amino Acids
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,162A
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/703,675
FILING DATE: 27-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 21-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: KARA, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-920-162A-1

Query Match 100.0%; Score 222; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 3.2e-27;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAFFRHDSGYEVHHQKLVFAEDVGSNKGALITGLMVGCVIAT 43
DB 1 DAFFRHDSGYEVHHQKLVFAEDVGSNKGALITGLMVGCVIAT 43

Search completed: October 31, 2002, 10:13:34
Job time : 2.16359 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:56 ; Search time 1.6925 Seconds
(without alignments)
2441.270 Million cell updates/sec

Title: US-09-785-215-2_COPY_672_714

Sequence: 1 DAEFRHDSGYEVHHQKLVFF.....VGSNKGAIIGLMVGVVIAT 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR.71.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	222	100.0	57	2	EC0045 Alzheimer's disease
2	222	100.0	57	2	EC0045 Alzheimer's disease
3	222	100.0	57	2	EC0045 Alzheimer's disease
4	222	100.0	57	2	EC0045 Alzheimer's disease
5	222	100.0	57	2	EC0045 Alzheimer's disease
6	222	100.0	57	2	EC0045 Alzheimer's disease
7	222	100.0	57	2	EC0045 Alzheimer's disease
8	222	100.0	57	2	EC0045 Alzheimer's disease
9	222	100.0	57	2	EC0045 Alzheimer's disease
10	217	97.7	42	2	EC0045 Alzheimer's disease
11	203	91.4	695	2	EC0045 Alzheimer's disease
12	203	91.4	695	2	EC0045 Alzheimer's disease
13	203	91.4	695	2	EC0045 Alzheimer's disease
14	133	59.9	733	2	EC0045 Alzheimer's disease
15	64	28.8	755	2	EC0045 Alzheimer's disease
16	62	27.9	755	2	EC0045 Alzheimer's disease
17	62	27.9	755	2	EC0045 Alzheimer's disease
18	57	25.7	327	2	EC0045 Alzheimer's disease
19	57	25.7	327	2	EC0045 Alzheimer's disease
20	56.5	25.5	378	2	EC0045 Alzheimer's disease
21	55.5	25.0	621	2	EC0045 Alzheimer's disease
22	55.5	25.0	621	2	EC0045 Alzheimer's disease
23	55.5	25.0	621	2	EC0045 Alzheimer's disease
24	55.5	25.0	621	2	EC0045 Alzheimer's disease
25	55	24.8	291	2	EC0045 Alzheimer's disease
26	55	24.8	317	2	EC0045 Alzheimer's disease
27	55	24.8	488	2	EC0045 Alzheimer's disease
28	55	24.8	738	2	EC0045 Alzheimer's disease
29	55	24.8	3063	2	EC0045 Alzheimer's disease

30	54.5	24.5	678	2	C81683 3-methyl-2-oxobuta
31	54.5	24.5	832	2	H84848 phospholipase D li
32	54	24.3	777	2	C97027 feoh-like protein,
33	54	24.3	284	2	S04723 genome polypeptide
34	54	24.3	316	2	D97865 hypothetical prote
35	54	24.3	322	2	E71647 hypothetical prote
36	54	24.3	763	2	A13443 Na+/H+ antiporter
37	53.5	24.1	245	2	AG1461 probable phospho-b
38	53.5	24.1	245	2	AH1098 a probable phospho
39	53.5	24.1	708	2	T24727 hypothetical prote
40	53.5	24.1	971	2	D70128 conserved hypotnet
41	53	23.9	256	2	G96774 hypothetical prote
42	53	23.9	390	2	C75103 Na+/H+ antiporter
43	53	23.9	422	2	D72302 hypothetical prote
44	53	23.9	601	2	T02581 nucleolin-like prote
45	53	23.9	1555	2	JT0959 polypeptide - pola

ALIGNMENTS

RESULT 1

EC0045 Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C:Species: Ovis sp. (sheep)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: EC0045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in (

A:Reference number: A60045; MUID:9201079

A:Accession: EC0045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56130

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein;

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.7e-22;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0y 1 DAEFRHDSGYEVHHQKLVFFADVGSNKGAIIGLMVGVVIAT 43

Db 6 DAEFRHDSGYEVHHQKLVFFADVGSNKGAIIGLMVGVVIAT 48

RESULT 2

EC0045 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999

C:Accession: EC0045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in (

A:Reference number: A60045; MUID:9201079

A:Accession: EC0045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56127; MUID:91895; PIDN:CA39592.1; PID:91896

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein;

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.7e-22;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0y 1 DAEFRHDSGYEVHHQKLVFFADVGSNKGAIIGLMVGVVIAT 43

Db 6 DAEFRHDSGYEVHHQKLVFFADVGSNKGAIIGLMVGVVIAT 48

RESULT 3

660045 Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 222; DB 2; Length 57;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAFFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
|||||
6 DAFFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 4

D60045 Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 100.0%; Score 222; DB 2; Length 57;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAFFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
|||||
6 DAFFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 5

A60045 Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2,7e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAFFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
|||||
DB 6 DAFFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 6

B60045 Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:92165; PIDN:CAA39593.1; PID:92166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 100.0%; Score 222; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2,7e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAFFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
|||||
DB 6 DAFFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 48

RESULT 7

P00438 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: P00438; G60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: P00438; MUID:93075180
A:Accession: P00438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83558; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 100.0%; Score 222; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 4,1e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAFFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
|||||
DB 17 DAFFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGVVIAT 59

RESULT 8

A49795 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlasky, M.B.; Toljan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991

A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
 A:Reference number: A49795; MUID:91273117
 A:Accession: A49795
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <POD>
 A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA56929.1; PID:g342063
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunlitz-type proteinase 1
 C:Keywords: alternative splicing

Query Match 100.0%; Score 222; DB 1; Length 695;
 Best Local Similarity 100.0%; Pred. No. 4,3e-21;
 Matches 43; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERFHDGSEVHHQKLVFAEDVGSNGKATIGLMVGGVIAT 43
 Db 597 DAERFHDGSEVHHQKLVFAEDVGSNGKATIGLMVGGVIAT 639

RESULT 9

Alzheimer's disease amyloid beta protein precursor [validated] - human
 A:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIIa inhibi
 N:Contents: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-1987 #sequence; revision 28-Jul-1995 #text; change 15-Sep-2000
 C:Accession: S02260; S05194; A32277; A32260; A35486; I39452; I39451; I39453; I59562; A44
 4666; A28503; A29302; A60805; J10038; S06121; A60355; A59011; A33884; S29076; S38252; S3
 R:Lemaire, H.G.; Salbaum, J.M.; Muthupai, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.; Bey
 Nucleic Acids Res. 17: 517-522, 1989
 A:Title: The PrecA(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
 A:Reference number: S02260; MUID:89128427
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288, 'V', 365-770 <LEM1>
 A:Cross-references: EMBL:X13466
 A>Note: alternative splice form APP(695)
 R:Lemaire, H.G.
 A:Title: alternative splice form APP(695)
 submitted to the EMBL Data Library, November 1988
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'V', 17-288, 'V', 365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:g353598; PIDN:CAA31830.1; PID:g871360
 A>Note: alternative splice form APP(695)
 R:La Pauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159: 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-prote
 A:Reference number: A32277; MUID:89165870
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LAF>
 A:Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AA31654.1; PID:g516074
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
 Biochem. Biophys. Res. Commun. 163: 1248-1253, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
 A:Reference number: A33260; MUID:89392030
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <JOH>
 A:Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
 R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
 Biochem. Biophys. Res. Commun. 170: 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
 A:Reference number: A35486; MUID:90321244
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PRE1>
 A>Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 87: 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.

A:Reference number: I39451; MUID:90236318
 A:Accession: I39452
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB,
 A:Molecule type: DNA
 A:Residues: 1-770 <YOS1>
 A:Cross-references: GB:M33112; NID:g178613; PIDN:AA59502.1; PID:g178616
 A:Accession: I39451
 A>Status: nucleic acid sequence not shown; translation not shown; translated from GB,
 A:Molecule type: DNA
 A:Residues: 1-530, 'QWLMPVIPAFAWEAKVGR' <YOS2>
 A:Cross-references: GB:M34875; NID:g178608; PIDN:AA59501.1; PID:g178615
 R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sasaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168
 A:Contents: annotation; extratum
 A>Note: revised physical map for reference I39451
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van D
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hem
 A:Reference number: I39453; MUID:90260663
 A:Accession: I39453
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
 A>Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzh
 A:Reference number: I59562; MUID:9022553
 A:Accession: I59562
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'F', 718-737 <MUR>
 A:Cross-references: GB:S57665; NID:g236720; PIDN:AA61991.1; PID:g236721
 R:Kamino, K.; Orr, H.T.; Payami, H.; Wajsbom, E.M.; Alonso, M.E.; Pulst, S.M.; Anders
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kikkuli, W.; Larson, E.; Heston, L.L.; Mart
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for 1
 A:Reference number: A44017; MUID:93035397
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-718 <KAN2>
 A:Cross-references: GB:S45136; NID:g257379; PIDN:AA623646.1; PID:g257380
 A:Experimental source: familial Alzheimer disease family 11T
 A>Note: sequence extracted from NCBI backbone (NCBI:P:115376)
 A:Note: this sequence has a silent mutation
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.
 Nature 325, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-su
 A:Reference number: A03134; MUID:87144572
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAN>
 A:Cross-references: GB:I00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
 A>Note: alternative splice form APP(695)
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascul
 A:Reference number: A29030; MUID:87231971
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A:Cross-references: GB:M46765; NID:g178539; PIDN:AAA51722.1; PID:g178540
 A>Note: the authors translated the codon GAG for residue 647 as Asp
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Safiotti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987

A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', 758-770 <GOL>
 A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
 A:Experimental source: brain
 R:Tanzil, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
 Science 235, 880-884, 1987
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
 A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TAN1>
 A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
 R:Dykes, T.; Weidemann, A.; Multhaupt, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mueller
 EMBO J. 7, 949-957, 1988
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pre
 A:Accession: S02638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DYK>
 R:Tanzil, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
 Nature 331, 528-530, 1988
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat
 A:Reference number: S00707; MUID:88122640
 A:Accession: S00707
 A:Molecule type: mRNA
 A:Residues: 286-344, 'I', 365-366 <TAN2>
 A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
 A:Experimental source: promyelocytic leukemia cell line HL60
 A:Note: alternative splice form APP(751)
 R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; De
 Nature 331, 525-527, 1988
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
 A:Reference number: S00925; MUID:88122639
 A:Accession: S00925
 A:Molecule type: mRNA
 A:Residues: 1-344, 'I', 365-366 <PO2>
 A:Cross-references: GB:X06989; EMBL:X00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
 A:Note: alternative splice form APP(751)
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
 A:Reference number: A38949; MUID:88122641
 A:Accession: A38949
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>
 A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
 A:Experimental source: glioblastoma cell line
 A:Note: alternative splice form APP(770)
 R:Vittek, M.P.; Rasool, C.G.; de Sauvage, F.; Vittek, S.M.; Battus, R.T.; Beer, B.; Ashton
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three F
 A:Reference number: A30320
 A:Accession: A30320
 A:Molecule type: mRNA
 A:Status: not compared with conceptual translation
 A:Residues: 284-288, 'V', 365-770 <VIT1>
 A:Accession: B30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 122-288, 'V', 365-770 <VIT2>
 A:Accession: C30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 606-770 <VIT3>
 R:Zelin, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.A
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease br
 A:Reference number: A31087; MUID:88124954
 A:Accession: A31087
 A:Molecule type: mRNA

A:Residues: 507-770 <ZAI>
 A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue
 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0
 R:Masters, C.L.; Multhaupt, G.; Simms, G.; Poltgieser, J.; Martins, R.N.; Beyreuther,
 Query Match 100.0%; Score 222; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 4, 8e-21;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEPFHDSGYEVHHQKLVFFAEDVGSNKGATIGLVGCVIAT 43
 DB 672 DAEPFHDSGYEVHHQKLVFFAEDVGSNKGATIGLVGCVIAT 714
 RESULT 10
 PN0512
 beta-amyloid protein - guinea pig (fragment)
 C:Species: Cavia porcellus (guinea pig)
 C>Date: 31-Dec-1993 #sequence, revision 31-Dec-1993 #text, change 17-Mar-1999
 C:Accession: PN0512
 R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno
 Biochem. Biophys. Res. Commun. 193, 624-630, 1993
 A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra
 A:Reference number: PN0512; MUID:93290653
 A:Accession: PN0512
 A:Molecule type: protein
 A:Residues: 1-42 <SHI>
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinas
 C:Keywords: alternative splicing; amyloid
 Query Match 97.7%; Score 217; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 8, 9e-22;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAEPFHDSGYEVHHQKLVFFAEDVGSNKGATIGLVGCVIAT 42
 DB 1 DAEPFHDSGYEVHHQKLVFFAEDVGSNKGATIGLVGCVIAT 42
 RESULT 11
 A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 C:Alternate names: proteinase nexin II
 C:Species: Mus musculus (house mouse)
 C>Date: 31-Mar-1989 #sequence, revision 31-Mar-1989 #text, change 13-Aug-1999
 C:Accession: A27485; S19727; I49485
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein pr
 A:Reference number: A27485; MUID:88106489
 A:Accession: A27485
 A:Molecule type: mRNA
 A:Residues: 1-695 <YAM>
 A:Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
 A:Experimental source: brain
 R:de Strooper, B.; van Leuven, F.; van den Bergh, H.
 Biochim. Biophys. Acta 1129, 141-143, 1991
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is clos
 A:Reference number: S19727; MUID:92096458
 A:Accession: S19727
 A:Molecule type: mRNA
 A:Residues: 1210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
 A:Cross-references: EMBL:X59379
 R:Izum, R.; Yamada, T.; Yoshikawa, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
 Gene 112, 189-195, 1992
 A:Title: Positive and negative regulatory elements for the expression of the Alzheimer
 A:Reference number: I49485; MUID:92209998
 A:Accession: I49485
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-19 <RES>

[illegible]

```

R:Okado, H.; Okamoto, H.
Biochem Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: development
A:Reference number: JH0773; MUID:93129227
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: CB:SS2417; NID:g263150; PID:AB24853.1; PID:g263151
A:Experimental source: Larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:287-337/Domains: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match      91.4%; Score 203; DB 2; Length 747;
Best Local Similarity 88.4%; Pred. No. 1,46-18;
Matches 38; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy      1 DAEFRHDSGYEVHHOKLVFAEDVGSNGKAITIGLVGVIAT 43
      1:||||: |||||||||:|||||||:|||||||:|||||||:
Db      649 DSEYRHDTAEVHHOKLVFAEDVGSNGKAITIGLVGVIAT 691

RESULT 14
S23094
beta-amyloid protein precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C:Accession: S23094
R:Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A:Reference number: S23094; MUID:92316198
A:Accession: S23094
A:Molecule type: Protein
A:Residues: 1-33 <KOJ>
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match      59.9%; Score 133; DB 2; Length 33;
Best Local Similarity 89.3%; Pred. No. 7,36-11;
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy      1 DAEFRHDSGYEVHHOKLVFAEDVGSNK 28
      |||||:|||||:|||||||:|||||||
Db      6 DAEFGHDSGFVEYRHOKLVFAEDVGSNK 33

RESULT 15
AI3228
tryptophan 2-monooxygenase tmsl [imported] - Agrobacterium tumefaciens (strain C58, tmsl)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C:Accession: AI3228
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Mochly, R.; Romero, P.; Zhang, S.;
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AI3228
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-755 <KUR>
A:Cross-references: GB:AE008690; PID:AL446247.1; PID:g17744025; GSPDB:GN00189
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: tmsl
A:Genome: plasmid
C:Superfamily: Agrobacterium plasmid tryptophan 2-monooxygenase

Query Match      28.8%; Score 64; DB 2; Length 755;
Best Local Similarity 43.2%; Pred. NO 2,6;

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Thu Oct 31 10:41:53 2002

us-09-785-2_copy_672_714.rpr

Page 6

Matches 16; Conservative 6; Mismatches 9; Indels 6; Gaps 1;

```

QY      7 DSGYEVIHQKLEVEFAEDVGSNKGAIIGLMVGVIAT 43
      III :: II III I IIII : I:I:I:
Db      223 DSG-----RIGFFPEDVPRKVAIIIGAGISGLVAS 253

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Search completed: October 31, 2002, 10:13:08
Job time : 4.6925 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:55 ; Search time 0.95203 Seconds
(without alignments)
1748.833 Million cell updates/sec

Title: US-09-785-215-2_COPY_672_714

Perfect score: 222
Sequence: 1 DAEPFRHDSGYEVHHOKLVEF.....VGSNKGALIGLWGVVIAT 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	222	100.0	57	A4_PIG	Q29023 sus scrofa
2	222	100.0	57	A4_UR5MA	Q29149 ursus marit
3	222	100.0	58	A4_CANFA	Q28280 canis famil
4	222	100.0	58	A4_RABIT	Q28748 oryctolagus
5	222	100.0	58	A4_SHEEP	Q28757 ovis aries
6	222	100.0	59	A4_BOVIN	Q28053 bos taurus
7	222	100.0	751	A4_SAISC	Q95541 salmistr sci
8	222	100.0	770	A4_HUMAN	P05067 homo sapien
9	203	91.4	770	A4_MOUSE	P12023 mus musculu
10	203	91.4	770	A4_RAT	P08592 rattus norv
11	62	27.9	755	TR2M_AGRV4	P04029 agrobacteri
12	62	27.9	755	TR2N_AGRV1	P25017 agrobacteri
13	57	25.7	327	POLG_PVYCH	P21294 potato vitu
14	57	25.7	503	Y226_MYCIN	P75462 mycoplasma
15	56.5	23.5	378	SLG1_YEAST	P34867 saccharomyc
16	55.5	23.0	297	FTF_ARCFU	Q28076 archaeglob
17	55	24.8	488	DHAL_PSESP	P33008 pseudomonas
18	55	24.8	3063	POLG_PVYN	P18897 p genome po
19	54	24.3	284	POLG_PVYVO	P11897 potato vitu
20	54	24.3	322	Y853_RICPR	O95ca7 rickettsia
21	53.5	24.1	708	YNRB_CABEL	P45972 caenorhabdi
22	53.5	24.1	971	Y228_BORBU	O51246 borrelia bu
23	52	23.4	1036	YCR3_YEAST	P25351 saccharomyc
24	51.5	23.2	611	PLD1_CRIGR	O08684 cricetus
25	51	23.0	494	COBO_MYCTU	O53677 mycobacteri
26	51	23.0	763	APP2_HUMAN	O06481 homo sapien
27	51	23.0	769	ITB2_BOVIN	P32592 bos taurus
28	50	22.5	285	MEMB_HABIN	P49960 haemophilus
29	50	22.5	674	TMU1_ARATH	P33343 arabidopsis
30	50	22.5	1437	MRP5_HUMAN	O15440 homo sapien
31	49.5	22.3	1162	11621_IBVM	P12651 avian infec
32	49	22.1	246	TPIS_CULFA	P30741 culicx tarsa
33	49	22.1	403	PGK_STRCO	O92519 streptomyce

34	49	22.1	542	1	YM87_MYCTU	O50678 mycobacteri
35	49	22.1	568	1	NIRS_PSEAE	P24474 pseudomonas
36	49	22.1	695	1	APP2_MOUSE	O06335 mus musculu
37	49	22.1	701	1	YGS1_YEAST	P53326 saccharomyc
38	49	22.1	704	1	SSP2_BOMO	P20613 bombyx mori
39	49	22.1	753	1	PPE2_HUMAN	O14830 homo sapien
40	49	22.1	757	1	PPE2_MOUSE	O35385 mus musculu
41	49	22.1	1080	1	HDC_DROME	O942m8 drosophila
42	48.5	21.8	160	1	FMDR_ECOLI	P24093 escherichia
43	48.5	21.8	330	1	COAT_PEW	P07993 pepper moti
44	48.5	21.8	393	1	GUN1_USTMA	P54424 ustilago ma
45	48.5	21.8	459	1	Y226_MYCSE	P47468 mycoplasma

ALIGNMENTS

RESULT 1	STANDARD	PRT	57 AA
A4_PIG			
ID	Q29023;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid		
DE	protein (Beta-Ap) (A-beta)] (Fragment).		
GN	APP.		
OS	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OX	NCBI_TaxID=9823;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=92017079; PubMed=1656157;		
RA	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;		
RT	"Conservation of the sequence of the Alzheimer's disease amyloid		
RT	peptide in dog, polar bear and five other mammals by cross-species		
RT	polymerase chain reaction analysis."		
RL	Brain Res. Mol. Brain Res. 10:299-305(1991).		
CC	- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO		
CC	INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN		
CC	G(O) (BY SIMILARITY).		
CC	- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	- SIMILARITY: BELONGS TO THE APP FAMILY.		
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@sib-sib.ch).		
CC	EMBL; X56127; CA39592.1; -		
DR	HSP6; P05067; IBA4.		
DR	InterPro; IPR001868; A4_APP.		
DR	PROSITE; PS00319; A4_EXTRA; PARTIAL.		
DR	PROSITE; PS00320; A4_INTRA; PARTIAL.		
KW	Glycoprotein; Amyloid; Neurone; Transmembrane.		
FT	NON_TER	1	
FT	CHAIN	6	48
FT	DOMAIN	<1	33
FT	TRANSMEM	34	57
FT	NON_TER	57	57
SO	SEQUENCE	57 AA; 6172 MW; 84209D88EBA82DFA CRC64;	
Query Match	100.0%;	Score 222; DB 1; Length 57;	
Best Local Similarity	100.0%;	Pred. No. 2.5e-22;	
Matches	43; Conservative	0; Mismatches	0; Indels
0;		Gaps	0;
1	DAEPFRHDSGYEVHHOKLVEFADVGSNKGALIGLWGVVIAT 43		

Db 6 DAEFRHDSGEYVHOKLVEFADVGSNKGAIIGLVGCVIAT 48

RESULT 2

A4_UR5MA STANDARD: PRT: 57 AA.

AC Q29149: MEDLINE=92017079; PubMed=1656157;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-Ap4) (A-beta)] (Fragment).

GN APP.

OS Ursus maritimus (Polar bear) (Thalartos maritimus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.

OX NCBI_TaxID=29073;

RN [1]

RP SEQUENCE FROM N.A.

RT TISSUE-Brain:

RT MEDLINE=92017079; PubMed=1656157;

RT Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species RT polymerase chain reaction analysis."

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).

CC -I- SUBCELLULAR LOCATION: Type I membrane protein.

CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -----

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CC -----

CC EMBL: X56128; CA39593.1; -.

DR HSSP: P05067; 1BA4.

DR InterPro: IPR001868; A4_APP.

DR PROSITE: PS00319; A4_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4_INTRA; PARTIAL.

KM Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1

FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 34 57 POTENTIAL.

FT NON_TER 57

FT SEQUENCE 57 AA: 6172 MW: 84209D868BA82DFA CRC64;

Query Match 100.0%; Score 222; DB 1; Length 57;

Best Local Similarity 100.0%; Pred. No. 2.5e-22;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEYVHOKLVEFADVGSNKGAIIGLVGCVIAT 43

Db 6 DAEFRHDSGEYVHOKLVEFADVGSNKGAIIGLVGCVIAT 48

RESULT 3

A4_CANFA STANDARD: PRT: 58 AA.

AC Q28280: MEDLINE=92017079; PubMed=1656157;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-Ap4) (A-beta)] (Fragment).

GN APP.

OS Canis familiaris (Dog).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RT TISSUE-Kidney:

RT MEDLINE=92017079; PubMed=1656157;

RT Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species RT polymerase chain reaction analysis."

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).

CC -I- SUBCELLULAR LOCATION: Type I membrane protein.

CC -I- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -----

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CC -----

CC EMBL: X56125; CA39590.1; -.

DR HSSP: P05067; 1BA4.

DR InterPro: IPR001868; A4_APP.

DR PROSITE: PS00319; A4_EXTRA; PARTIAL.

DR PROSITE: PS00320; A4_INTRA; PARTIAL.

KM Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1

FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 35 58 POTENTIAL.

FT NON_TER 58

FT SEQUENCE 58 AA: 6285 MW: 8469D488A2E12DFA CRC64;

Query Match 100.0%; Score 222; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 2.6e-22;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEYVHOKLVEFADVGSNKGAIIGLVGCVIAT 43

Db 7 DAEFRHDSGEYVHOKLVEFADVGSNKGAIIGLVGCVIAT 49

RESULT 4

A4_RABIT STANDARD: PRT: 58 AA.

AC Q28748: MEDLINE=92017079; PubMed=1656157;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-Ap4) (A-beta)] (Fragment).

GN APP.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RT TISSUE-Brain:

RT MEDLINE=92017079; PubMed=1656157;

RT Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species RT polymerase chain reaction analysis."

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

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CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X56129; CAA39594.1; -.
DR      HSSP: P05067; 1BA4.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1
FT      CHAIN      1 48      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN      <1 33      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      34 57      POTENTIAL.
FT      DOMAIN      58 >58      CYTOPLASMIC (POTENTIAL).
FT      NON_TER      58 58
SQ      SEQUENCE      58 AA: 6300 MM: F434209D88BBA82D CRC64;

Query Match      100.0%; Score 222; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGATITGLMVGCVIAT 43
DB      6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGATITGLMVGCVIAT 48

RESULT 5
A4_SHEEP
ID      A4_SHEEP      STANDARD:      PRT:      58 AA.
AC      Q28757;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-APP) (A-beta)] (Fragment).
CN      APP.
OS      Ovis aries (Sheep).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Caprinae; Ovis.
X      NCB1_TaxID=9940;
X      [1]
X      SEQUENCE FROM N.A.
X      TISSUE=Heart;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      -----

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DR      EMBL: X56130; CAA39595.1; -.
DR      HSSP: P05067; 1AHL.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1
FT      CHAIN      1 48      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN      <1 33      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      34 57      POTENTIAL.
FT      DOMAIN      58 >58      CYTOPLASMIC (POTENTIAL).
FT      NON_TER      58 58
SQ      SEQUENCE      58 AA: 6300 MM: F434209D88BBA82D CRC64;

Query Match      100.0%; Score 222; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGATITGLMVGCVIAT 43
DB      6 DAEFRHDSGYEVHHQKLVFAEDVGSNKGATITGLMVGCVIAT 48

RESULT 6
A4_BOVIN
ID      A4_BOVIN      STANDARD:      PRT:      59 AA.
AC      Q28053;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE      protein (Beta-APP) (A-beta)] (Fragment).
CN      APP.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
X      NCB1_TaxID=9913;
X      [1]
X      SEQUENCE FROM N.A.
X      TISSUE=Brain;
RX      MEDLINE=92017079; PubMed=1656157;
RA      Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT      "Conservation of the sequence of the Alzheimer's disease amyloid
RT      peptide in dog, polar bear and five other mammals by cross-species
RT      polymerase chain reaction analysis.";
RL      Brain Res. Mol. Brain Res. 10:299-305(1991).
CC      -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC      INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC      G(O) (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X56124; CAA39589.1; -.
DR      EMBL: X56126; CAA39591.1; -.
DR      HSSP: P05067; 1BA4.
DR      InterPro: IPR001868; A4_APP.
DR      PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR      PROSITE: PS00320; A4_INTRA; PARTIAL.
KW      Glycoprotein; Amyloid; Neurone; Transmembrane.
FT      NON_TER      1
FT      CHAIN      1 49      BETA-AMYLOID PROTEIN (POTENTIAL).
FT      DOMAIN      <1 34      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      35 58      POTENTIAL.
FT      DOMAIN      59 >59      CYTOPLASMIC (POTENTIAL).

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FT NON_TER 59 59
SQ SEQUENCE 59 AA: 6414 MW: F43469DA8A2E12D CRC64;
Query Match 100.0%; Score 222; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNGKGAITGLWGVVIAT 43
Db 7 DAEFRHDSGYEVHHOKLVFAEDVGSNGKGAITGLWGVVIAT 49
RESULT 7
A4_SAISC STANDARD: PRT: 751 AA.
AC 095241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-amyloid protein (Beta-ApP) (A-beta)].
OS Salimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Salimiri.
NCBI_TaxID=9521;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy".
RL Neurobiol. Aging 16:805-808(1995).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NEXT MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC
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CC
CC EMBL; S81024; AAD14347.1; -;
DR HSPB; P05067; IAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PRO0203; AMYLOIDA4.
DR PRINTS: PRO0759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS02279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
FT

FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 681 704 POTENTIAL.
FT DOMAIN 705 751 CYTOSOLASMIC (POTENTIAL).
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
FT ACT_SITE 301 302 REACTIVE BOND..
FT DISULFID 291 341 BY SIMILARITY.
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 751 AA; 84893 MW; 6C3EA31089569049 CRC64;
Query Match 100.0%; Score 222; DB 1; Length 751;
Best Local Similarity 100.0%; Pred. No. 3.6e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 DAEFRHDSGYEVHHOKLVFAEDVGSNGKGAITGLWGVVIAT 43
Db 653 DAEFRHDSGYEVHHOKLVFAEDVGSNGKGAITGLWGVVIAT 695
RESULT 8
A4_HUMAN STANDARD: PRT: 770 AA.
ID A4_HUMAN
AC P05067; P09000; Q16011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (PN-II) (APPI) [Contains: Beta-amyloid protein (beta-ApP) (A-beta)].
GN APP OR A4 OR CVAP OR AD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grieschlik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor".
RL Nature 325:733-736(1987).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine protease inhibitors".
RL Nature 331:525-527(1988).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The preA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons".
RL Nucleic Acids Res. 17:517-522(1989).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M., Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for sequencing of a 300 kb region of human APP locus".
RL Nucleic Acids Res. 25:1802-1808(1997).
[5]
RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RX

RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.: "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease."; *Proc. Natl. Acad. Sci. U.S.A.* 84:4190-4194(1987).
RN Nature 331:528-530(1988).
[6]
RX MEDLINE=88122641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.:
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity."; *Proc. Natl. Acad. Sci. U.S.A.* 84:4190-4194(1987).
RN Nature 331:530-532(1988).
[7]
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.:
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides."; *Proc. Natl. Acad. Sci. U.S.A.* 84:4190-4194(1987).
RN [8]
RX MEDLINE=88124954; PubMed=2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marcotta C.A.:
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex."; *Proc. Natl. Acad. Sci. U.S.A.* 85:929-933(1988).
RN [9]
RX MEDLINE=88035004; PubMed=3312495;
RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RA Tontellotte W.W., Heubner V., Shively J.E.:
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
RT and partial sequence of a 4,200-dalton peptide isolated from cortical
RT microvessels."; *J. Neurochem.* 49:1394-1401(1987).
RN [10]
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikawa S.-I., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.:
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene."; *Gene* 87:257-263(1990).
RN [11]
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.:
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide."; *Nucleic Acids Res.* 16:9351-9351(1988).
RN [12]
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.:
RT "Purification of protease nexin II from human fibroblasts."; *J. Biol. Chem.* 262:8508-8514(1987).
RN [13]
RX MEDLINE=89384866; PubMed=2506449;
RA Oltersdorf T., Fritze L.C., Schenk D.B., Lieberburg I.,
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
RA Sinha S.:
RT "The secreted form of the Alzheimer's amyloid precursor protein with
RT the Kunitz domain is protease nexin-II."; *Nature* 341:144-147(1989).
RN [14]
RX MEDLINE=90211252; PubMed=1969731;
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.:
RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
RT disease amyloid protein precursor."; *Biochem. Biophys. Res. Commun.* 167:716-721(1990).
RN [15]
RX MEDLINE=93188965; PubMed=8446172;
RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
RA Murayama Y., Ogata E.:
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
RT protein G(0)"; *Nature* 362:75-79(1993).
RN [16]
RX MEDLINE=99215582; PubMed=10201399;
RA Rossjohn J., Cappai R., Fell S.C., Henry A., McKinsty W.J.,
RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
RA Parker M.W.:
RT "Crystal structure of the N-terminal, growth factor-like domain of
RT Alzheimer amyloid precursor protein"; *Nat. Struct. Biol.* 6:327-331(1999).
RN [17]
RX MEDLINE=91104913; PubMed=2125487;
RA Hynes T.R., Randel M., Kennedy L.A., Eisenbrodt C., Kossiakof A.A.:
RT "X-ray crystal structure of the protease inhibitor domain of
RT Alzheimer's amyloid beta-protein precursor."; *Biochemistry* 29:10018-10022(1990).
RN [18]
RX MEDLINE=94281210; PubMed=7516706;
RA Talarious J., Marciniowski K.J., Klopman G., Zagorski M.G.:
RT "Solution structure of residues 1-28 of the amyloid beta-peptide."; *Biochemistry* 33:7788-7796(1994).
RN [20]
RX MEDLINE=97128622; PubMed=8973180;
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.:
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
RT membrane-mimicking environment."; *Biochemistry* 35:16094-16104(1996).
RN [21]
RX MEDLINE=98359783; PubMed=9693002;
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.:
RT "Solution structure of amyloid beta-peptide(1-40) in a water-miscible
RT environment. Is the membrane-spanning domain where we think it is?"; *Biochemistry* 37:11064-11077(1998).
RN [22]
RX MEDLINE=20400065; PubMed=10940222;
RA Poulsen S.-A., Watson A.A., Craik D.J.:
RT "Solution structures in aqueous SDS micelles of two amyloid beta
RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
RT site."; *Struct. Biol.* 130:142-152(2000).
RN [23]
RX MEDLINE=20400065; PubMed=10940221;
RA Zhang S., Iwata K., Lachemann M.J., Peng J.W., Li S., Stimson E.R.,
RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.:
RT "The Alzheimer's peptide A beta adopts a collapsed coil structure in
RT water."; *Struct. Biol.* 130:130-141(2000).
RN [24]
RX SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.

DB 672 DAFFGHDGSEYVHOKLVEFAEDVGSNKGAIIGLMVGVYAT 714

RESULT 10

AA_RAT STANDARD: PRT: 770 AA.

ID A4_RAT

AC P08592:

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog precursor (Amyloidogenic glycoprotein) (AG).

GN APP.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.

RC TISSUE=Brain;

RA MEDLINE=86312583; PubMed=2900758;

RA Shivers B.D., Hilbich C., Multaup G., Salbaum J.M., Beyreuther K., Seeburg P.H.;

RA "Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brain suggests a role in cell contact.";

RT EMO J. 7:1365-1370(1988).

RL [2]

RN SEQUENCE OF 289-364 FROM N.A.

RC TISSUE=Liver;

RA MEDLINE=89183625; PubMed=2648331;

RA Kang J., Mueller-Hill B.;

RA "The sequence of the two extra exons in rat pre4.";

RL Nucleic Acids Res. 17:2130-2130(1989).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695), APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, BETA, AND GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

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CC EMBL; X07648; CAA30488.1; -

DR EMBL; X14066; CAA32229.1; -

DR PIR; S00550; S00550.

DR PIR; S03607; S03607.

DR HSP; F05067; IAAp.

DR InterPro; IPR001868; A4_APP.

DR InterPro; IPR002223; Kunitz_BPTI.

DR Pfam; PF021177; A4_EXTRA; 1.

DR Pfam; PF00014; Kunitz_BPTI; 1.

DR PRINTS; PR00203; AMYLOIDA4.

DR PRINTS; PR00759; BASICPTASE.

DR SMART; SM00006; A4_EXTRA; 1.

DR SMART; SM00131; KU; 1.

DR PROSITE; PS00319; A4_EXTRA; 1.

DR PROSITE; PS00320; A4_INTRA; 1.

DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.

KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;

KW Alternative splicing; Serine protease inhibitor.

FT SIGNAL 1 17 BY SIMILARITY.

FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN

FT HOMOLOG.

FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 700 723 POTENTIAL.

FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 673 715 EQUIVALENT OF BETA-AMYLOID PROTEIN.

FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.

FT SITE 759 762 CLATHRIN-BINDING (BY SIMILARITY).

FT DISULFID 291 341 BY SIMILARITY.

FT DISULFID 300 324 BY SIMILARITY.

FT DISULFID 316 337 BY SIMILARITY.

FT CARBOHYD 542 542 N-LINKED (GLCNAc. . .) (POTENTIAL).

FT CARBOHYD 571 571 N-LINKED (GLCNAc. . .) (POTENTIAL).

FT VARSPIC 289 289 E -> V (IN ISOFORM APP(695)).

FT VARSPIC 290 364 MISSING (IN ISOFORM APP(695)).

SO SEQUENCE 770 AA; 86704 MW; C26C9D6BBD929A7 CRC64.

Query Match 91.4%; Score 203; DB 1; Length 770;

Best Local Similarity 93.0%; Pred. No. 1;le-18;

Matches 40; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DAFFRHDGSEYVHOKLVEFAEDVGSNKGAIIGLMVGVYAT 43

DB 672 DAFFGHDGSEYVHOKLVEFAEDVGSNKGAIIGLMVGVYAT 714

RESULT 11

TR2M_AGR4

ID TR2M_AGR4 STANDARD: PRT: 755 AA.

AC P04029;

DT 23-OCT-1986 (Rel. 02, Created)

DT 23-OCT-1986 (Rel. 02, Last sequence update)

DT 13-DEC-1998 (Rel. 37, Last annotation update)

DE Tryptophan 2-monooxygenase (EC 1.13.12.3).

GN Tms1.

OS Agrobacterium tumefaciens.

OG Plasmid pTiAch5, and plasmid pTiA6NC.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OX Rhizobiaceae; Rhizobium.

CC NCBI_TaxID=358;

CC [1]

CC SEQUENCE FROM N.A.

CC PLASMID-pTiAch5;

CC MEDLINE=84207942; PubMed=6327292;

CC Gietlen J., de Beuckeleer M., Seutinck J., Deboeck F., de Greve H., Lemmers M., van Montagu M., Scheil J.;

CC "The complete nucleotide sequence of the TL-DNA of the Agrobacterium tumefaciens plasmid pTiAch5.";

CC EMO J. 3:835-846(1984).

CC [2]

CC SEQUENCE FROM N.A.

CC PLASMID-pTiA6NC;

CC MEDLINE=84170374; PubMed=6584906;

CC Klee H., Montoya A., Horodyski F., Lichtenstein C., Garfinkel D., Fuller S., Flores C., Peschon J., Nester E., Gordon M.;

CC "Nucleotide sequence of the tms genes of the pTiA6NC octopine T1 plasmid: two gene products involved in plant tumorigenesis.";

CC Proc. Natl. Acad. Sci. U.S.A. 81:1728-1732(1984).

CC -1- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide + CO(2) + H(2)O.

CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF AUKINS FROM TRYPTOPHAN.

CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF ACH5.

CC -1- SIMILARITY: SIGNIFICANT HOMOLOGY TO THE ADENINE BINDING REGION OF P-HYDROXYBENZONATE HYDROXYLASE FROM P. FLUORESCENS. IT SEEMS THAT THIS PROTEIN BINDS ADENINE EITHER AS SUBSTRATE OR COFACTOR.

CC -1- SIMILARITY: STRONG, WITH ITS A. TUMEFACIENS PLASMID PTITM4 COUNTERPART.

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RESULT 14
Y226_MYCPN STANDARD: PRT: 503 AA.
AC ID Y226_MYCPN
AC P75462;
DT 01-NOV-1997 (Rel. 35, Created).
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG226 homolog (F10_crf503).
GN MP319 OR MP517.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
FA Himmelfreith R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
FA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae."
RT Nucleic Acids Res. 24:4420-4449(1996).
CC -1 SURCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1 SIMILARITY: TO M.GENITALINUM MG223.
CC -----
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CC -----
DR EMBL: AE000051; AAB9165.1;
DR InterPro: IPR002293; AA_rel-permease.1.
DR InterPro: IPR002027; Amino_acid-permease.
DR Pfam: PF00324; aa-permeases; 1.
DR KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 20 40 POTENTIAL.
FT TRANSMEM 43 63 POTENTIAL.
FT TRANSMEM 106 126 POTENTIAL.
FT TRANSMEM 138 158 POTENTIAL.
FT TRANSMEM 166 186 POTENTIAL.
FT TRANSMEM 215 235 POTENTIAL.
FT TRANSMEM 249 269 POTENTIAL.
FT TRANSMEM 301 321 POTENTIAL.
FT TRANSMEM 359 379 POTENTIAL.
FT TRANSMEM 405 425 POTENTIAL.
FT TRANSMEM 443 463 POTENTIAL.
FT TRANSMEM 468 488 POTENTIAL.
SO SEQUENCE 503 AA; 54960 MW; 4BC1BFDE036985B2 CnC64;

Query Match 25.7%; Score 57; DB 1; Length 503;
Best Local Similarity 61.1%; Pred. No. 6.1;
Matches 11; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 24 VGSNKGAIITGLMGVCVIT 41
I I I I I I I I I I I
DB 131 VKDNGALITGLVGGFVL 148

RESULT 15
SLGI_YEAST STANDARD: PRT: 378 AA.
AC ID SLGI_YEAST
AC P54867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1997 (Rel. 35, Last annotation update)
DE SLGI protein precursor
GN SLGI OR YOR008C OR UNE378.
OS Saccharomyces cerevisiae (Baker's yeast).

```

```

CC Eukaryota: Fungi: Ascomycota: Saccharomycotina: Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
CX NCBI_TaxID=4932;
RN [1]
RA de Bettignies G., Bergez-Aulio P., Barthe C., Louvet O.,
RA Peydouquet M.F., Morel C., Dolignon F., Crouzet M.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RA MEDLINE=97051599; PubMed=8896276;
RA Sterky F., Holmberg A., Pettersson B., Uhlen M.;
RT "The sequence of a 30 kb fragment on the left arm of chromosome XV
RT from Saccharomyces cerevisiae reveals 15 open reading frames, five of
RT which correspond to previously identified genes.";
RL Yeast 12:1091-1095(1996).
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CC -----
DR EMBL: U39481; AAA85862.1; -;
DR EMBL: U43491; AAC49488.1; -;
DR EMBL: Z74916; CAAG9196.1; -;
DR HSSP: P05067; 1BA6.
DR SCD: S0005534; SLG1.
DR InterPro: IPR002889; WSC.
DR Pfam: PF01822; WSC; 1.
DR SMART: SM00321; WSC; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1
FT CHAIN 19
FT CARBOHYD 65 378
FT CARBOHYD 354 354
FT SEQUENCE 378 AA; 39270 MW; EE616F2774CCCE3 CMC64;
RN [1]
RA de Bettignies G., Bergez-Aulio P., Barthe C., Louvet O.,
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DR EMBL: U39481; AAA85862.1; -;
DR EMBL: U43491; AAC49488.1; -;
DR EMBL: Z74916; CAAG9196.1; -;
DR HSSP: P05067; 1BA6.
DR SCD: S0005534; SLG1.
DR InterPro: IPR002889; WSC.
DR Pfam: PF01822; WSC; 1.
DR SMART: SM00321; WSC; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1
FT CHAIN 19
FT CARBOHYD 65 378
FT CARBOHYD 354 354
FT SEQUENCE 378 AA; 39270 MW; EE616F2774CCCE3 CMC64;
RN [1]
RA de Bettignies G., Bergez-Aulio P., Barthe C., Louvet O.,
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RA Sterky F., Holmberg A., Pettersson B., Uhlen M.;
RT "The sequence of a 30 kb fragment on the left arm of chromosome XV
RT from Saccharomyces cerevisiae reveals 15 open reading frames, five of
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DR EMBL: U39481; AAA85862.1; -;
DR EMBL: U43491; AAC49488.1; -;
DR EMBL: Z74916; CAAG9196.1; -;
DR HSSP: P05067; 1BA6.
DR SCD: S0005534; SLG1.
DR InterPro: IPR002889; WSC.
DR Pfam: PF01822; WSC; 1.
DR SMART: SM00321; WSC; 1.
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FT SIGNAL 1
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FT CARBOHYD 65 378
FT CARBOHYD 354 354
FT SEQUENCE 378 AA; 39270 MW; EE616F2774CCCE3 CMC64;
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RA Peydouquet M.F., Morel C., Dolignon F., Crouzet M.;
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DR EMBL: U39481; AAA85862.1; -;
DR EMBL: U43491; AAC49488.1; -;
DR EMBL: Z74916; CAAG9196.1; -;
DR HSSP: P05067; 1BA6.
DR SCD: S0005534; SLG1.
DR InterPro: IPR002889; WSC.
DR Pfam: PF01822; WSC; 1.
DR SMART: SM00321; WSC; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1
FT CHAIN 19
FT CARBOHYD 65 378
FT CARBOHYD 354 354
FT SEQUENCE 378 AA; 39270 MW; EE616F2774CCCE3 CMC64;
RN [1]
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RA Peydouquet M.F., Morel C., Dolignon F., Crouzet M.;
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RA Sterky F., Holmberg A., Pettersson B., Uhlen M.;
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RL Yeast 12:1091-1095(1996).
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DR EMBL: U39481; AAA85862.1; -;
DR EMBL: U43491; AAC49488.1; -;
DR EMBL: Z74916; CAAG9196.1; -;
DR HSSP: P05067; 1BA6.
DR SCD: S0005534; SLG1.
DR InterPro: IPR002889; WSC.
DR Pfam: PF01822; WSC; 1.
DR SMART: SM00321; WSC; 1.
KW Glycoprotein; Signal.
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FT CARBOHYD 65 378
FT CARBOHYD 354 354
FT SEQUENCE 378 AA; 39270 MW; EE616F2774CCCE3 CMC64;
RN [1]
RA de Bettignies G., Bergez-Aulio P., Barthe C., Louvet O.,
RA Peydouquet M.F., Morel C., Dolignon F., Crouzet M.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
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RN [2]
RA MEDLINE=97051599; PubMed=8896276;
RA Sterky F., Holmberg A., Pettersson B., Uhlen M.;
RT "The sequence of a 30 kb fragment on the left arm of chromosome XV
RT from Saccharomyces cerevisiae reveals 15 open reading frames, five of
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RL Yeast 12:1091-1095(1996).
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DR EMBL: U43491; AAC49488.1; -;
DR EMBL: Z74916; CAAG9196.1; -;
DR HSSP: P05067; 1BA6.
DR SCD: S0005534; SLG1.
DR InterPro: IPR002889; WSC.
DR Pfam: PF01822; WSC; 1.
DR SMART: SM00321; WSC; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1
FT CHAIN 19
FT CARBOHYD 65 378
FT CARBOHYD 354 354
FT SEQUENCE 378 AA; 39270 MW; EE616F2774CCCE3 CMC64;
RN [1]
RA de Bettignies G., Bergez-Aulio P., Barthe C., Louvet O.,
RA Peydouquet M.F., Morel C., Dolignon F., Crouzet M.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
[2]
RN [2]
RA MEDLINE=97051599; PubMed=8896276;
RA Sterky F., Holmberg A., Pettersson B., Uhlen M.;
RT "The sequence of a 30 kb fragment on the left arm of chromosome XV
RT from Saccharomyces cerevisiae reveals 15 open reading frames, five of
RT which correspond to previously identified genes.";
RL Yeast 12:1091-1095(1996).
CC -----
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CC -----
DR EMBL: U39481; AAA85862.1; -;
DR EMBL: U43491; AAC49488.1; -;
DR EMBL: Z74916; CAAG9196.1; -;
DR HSSP: P05067; 1
```

Search completed: October 31, 2002, 10:12:27
Job time : 3.95203 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:56 ; Search time 2.69742 Seconds
(without alignments)
2757.743 Million cell updates/sec

Title: US-09-785-215-2_COPY_672_714

Perfect score: 222
Sequence: 1 DAERRDSDGVEVHKKLVFF.....VGSNKAITGLMGVVIAT 43

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	222	100.0	82	4	P78438
2	222	100.0	82	4	P78438
3	222	100.0	82	4	P78438
4	222	100.0	82	4	P78438
5	222	100.0	82	4	P78438
6	222	100.0	82	4	P78438
7	222	100.0	82	4	P78438
8	222	100.0	82	4	P78438
9	222	100.0	82	4	P78438
10	222	100.0	82	4	P78438
11	222	100.0	82	4	P78438
12	222	100.0	82	4	P78438
13	222	100.0	82	4	P78438
14	222	100.0	82	4	P78438
15	222	100.0	82	4	P78438
16	222	100.0	82	4	P78438

17	203	91.4	747	13	091963	091963 xenopus. ap
18	200	90.1	695	13	0985F9	0985F9 xenopus lae
19	193	86.9	699	13	057394	057394 narke japon
20	180	81.1	780	13	073683	073683 tetraodon f
21	176	79.3	33	4	090C33	090C33 homo sapien
22	176	79.3	737	13	093279	093279 fugu rubrip
23	162.5	73.2	612	13	0919E7	0919E7 brachydanio
24	162.5	73.2	738	13	090W28	090W28 brachydanio
25	162	73.0	30	4	090CA9	090CA9 homo sapien
26	147	66.2	28	4	090CD1	090CD1 homo sapien
27	147	66.2	49	6	097917	097917 bos taurus
28	106	47.7	19	4	090CC8	090CC8 homo sapien
29	106	47.7	20	4	090CB6	090CB6 homo sapien
30	64	28.8	328	2	09RPS4	09RPS4 enterococcu
31	64	28.8	755	2	09R694	09R694 agrobacteri
32	64	28.8	755	2	09R717	09R717 agrobacteri
33	64	28.8	755	2	09R472	09R472 agrobacteri
34	62	27.9	755	2	044388	044388 agrobacteri
35	61	27.5	755	2	09WMA1	09WMA1 agrobacteri
36	57.5	25.9	895	10	09AMB6	09AMB6 lycopersico
37	57	25.7	195	10	022662	022662 arabidopsis
38	57	25.7	332	12	09DQ05	09DQ05 potato viru
39	57	25.7	365	12	09MG05	09MG05 potato viru
40	57	25.7	575	10	081120	081120 lotus japon
41	55.5	25.0	678	16	084344	084344 chlamydia t
42	55	24.8	291	16	097723	097723 streptococc
43	55	24.8	738	16	092VF1	092VF1 thizobium m
44	54.5	24.5	678	16	09PK54	09PK54 chlamydia m
45	54.5	24.5	829	10	09XG70	09XG70 gossypium h

ALIGNMENTS

RESULT 1

P78438	PRELIMINARY:	PRT:	82 AA.
AC	P78438.		
DT	01-MAY-1997 (TREMBLrel. 03, Created)		
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).		
GN	APP.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=89392030; PubMed=2675837;		
RA	Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,		
RA	Little S.P.;		
RT	"Alzheimer's disease amyloid peptide is encoded by two exons and shows		
RT	similarity to soybean trypsin inhibitor."		
RL	Biochem. Biophys. Res. Commun. 163:1248-1255(1989).		
RN	[2]		
RP	SEQUENCE OF 19-48 FROM N.A.		
RP	MEDLINE=87120329; PubMed=2949367;		
RA	Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,		
RA	Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;		
RT	"Amyloid beta protein gene: cDNA, mRNA distribution, and genetic		
RT	linkage near the Alzheimer locus."		
RL	Science 235:880-884(1987).		
RN	[3]		
RP	SEQUENCE OF 32-63 FROM N.A.		
RP	MEDLINE=9035397; PubMed=1415269;		
RA	Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M.,		
RA	Anderson L., O'dahl S., Nemens E., White J.A.;		
RT	"Linkage and mutational analysis of familial Alzheimer disease		
RT	kindreds for the APP gene region."		
RL	Am. J. Hum. Genet. 51:998-1014(1992).		
DR	EMBL: M29270; AAA51768.1; -;		
DR	EMBL: M29269; AAA51768.1; JOINED.		

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DR EMBL: M15532; AAA51564.1; -
DR EMBL: S45136; AAB23646.1; -
DR HSSP; P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATITGLMWGCVIAT 43
    |||||||
Db 17 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATITGLMWGCVIAT 59

RESULT 2
ID Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Blochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2; -
DR HSSP; P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATITGLMWGCVIAT 43
    |||||||
Db 18 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATITGLMWGCVIAT 60

RESULT 3
ID Q16019 PRELIMINARY; PRT; 82 AA.
AC Q16019;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Blochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; AAB26264.2; -
DR HSSP; P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;
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SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATITGLMWGCVIAT 43
    |||||||
Db 18 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATITGLMWGCVIAT 60

RESULT 4
ID Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Blochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61383; AAB26265.2; -
DR HSSP; P05067; 1BA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATITGLMWGCVIAT 43
    |||||||
Db 18 DAEFRHDSGYEVHHOKLVEFAEDVGSNKGATITGLMWGCVIAT 60

RESULT 5
ID Q93296 PRELIMINARY; PRT; 534 AA.
AC Q93296;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_Taxid=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan G.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYLOIDA4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
```

FT NON_TER 1 1
SQ SEQUENCE 534 AA: 60597 MW: FB53ECC2E66D4C92 CRC64:

Query Match 100.0%; Score 222; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 43
DB 436 DAEFRHDSGEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 478

RESULT 6

O95KN7 PRELIMINARY: PRT: 695 AA.

AC O95KN7
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crab eating macaque) (Cynomolpus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlasy M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease";
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL: M58727; AAA36829.1; -
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 597 636
SQ SEQUENCE 695 AA: 78663 MW: 4F6EA0139F69D56 CRC64;

Query Match 100.0%; Score 222; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 43
DB 597 DAEFRHDSGEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 639

RESULT 7

O60496 PRELIMINARY: PRT: 695 AA.

AC O60496
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in guinea pigs - complete cDNA sequence and
RT alternative splicing";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL: X97631; CA66230.1; -
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.

DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_EXTRA; 1.
SQ SEQUENCE 695 AA: 78701 MW: 5196A0C4017F16AB CRC64:

Query Match 100.0%; Score 222; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 43
DB 597 DAEFRHDSGEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 639

RESULT 8

O9DGJ8 PRELIMINARY: PRT: 695 AA.

AC O9DGJ8
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolose A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms";
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF289218; AAG00593.1; -
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
SQ SEQUENCE 695 AA: 78565 MW: F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 222; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 43
DB 597 DAEFRHDSGEVHHOKLVEFAEDVGSNKGAIIGLMVGVVIAT 639

RESULT 9

O9DGJ7 PRELIMINARY: PRT: 751 AA.

AC O9DGJ7
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolose A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms";
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF289219; AAG00594.1; -
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.

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DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR Serine protease inhibitor.
SQ SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 100.0%; Score 222; DB 13; Length 751;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIAT 43
DB 653 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIAT 695
RESULT 10
Q9TUI0 PRELIMINARY; PRT; 770 AA.
ID Q9TUI0
AC Q9TUI0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB032550; BAA84580.1; -.
DR HSSP: P05067; 1AA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BC583E CRC64;

Query Match 100.0%; Score 222; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIAT 43
DB 672 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIAT 714
RESULT 11
Q9PVL1 PRELIMINARY; PRT; 569 AA.
ID Q9PVL1
AC Q9PVL1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN APP.
```

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OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaeoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RA Coulson E.J., Paliaga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function."
RL Neurochem. Int. 0:0-0(2000).
DR EMBL: AF030341; AAF12698.1; -.
DR HSSP: P05067; 1AA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0ABBB851863A19D CRC64;

Query Match 97.7%; Score 217; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 4.9e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIAT 42
DB 472 DAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIAT 513
RESULT 12
Q13778 PRELIMINARY; PRT; 97 AA.
ID Q13778
AC Q13778;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=87120328; PubMed=3810169;
RA Goldgaber D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
RT brain amyloid of Alzheimer's disease."
RL Science 235:877-880(1987).
DR EMBL: M15533; AAB35540.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR PRINTS: PR00203; AMYLOIDA4.
DR NON_TER 1
SQ SEQUENCE 97 AA; 10884 MW; E528CDB448DE474E CRC64;

Query Match 95.5%; Score 212; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.9e-20;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIAT 43
DB 1 EFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIAT 41
RESULT 13
Q35463 PRELIMINARY; PRT; 79 AA.
ID Q35463
AC Q35463;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
```

DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).
 GN BETA APP.
 OS Crictulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Crictulus.
 NC NCBL_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sambamurti K., Plinix I., Gandhi S.;
 RL Submitted (OCr-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF030413; AAB86608.1; -
 DR HSSP; P05067; 1BA4.
 FT NON_TER 1 79
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BF3F597 CRC64;

Query Match 91.4%; Score 203; DB 11; Length 79;
 Best Local Similarity 93.0%; Pred. No. 3.4e-19;
 Matches 40; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEVHHOKLVFEADVGSNKGAIIIGLWGVVIAT 43
 DB 21 DAEFGHDSGEVHHOKLVFEADVGSNKGAIIIGLWGVVIAT 63

RESULT 14
 O99K32 PRELIMINARY; PRT; 607 AA.
 AC O99K32;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE HYPOTHEICAL 68.4 KDA PROTEIN (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NC NCBL_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MAMMARY TUMOR. MAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
 RC TISSUE;
 RA Strausberg R;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC005490; AAH05490.1; -
 DR HSSP; P05067; 1AAP.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF00014; Kunitz_BPTI.1.
 DR PRINTS; PRO0203; AMYLOIDA4.
 DR PRINTS; PRO0759; BASICPTASE.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KM Hypothetical protein; Serine protease inhibitor.
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

Query Match 91.4%; Score 203; DB 11; Length 607;
 Best Local Similarity 93.0%; Pred. No. 3.6e-18;
 Matches 40; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEVHHOKLVFEADVGSNKGAIIIGLWGVVIAT 43
 DB 509 DAEFGHDSGEVHHOKLVFEADVGSNKGAIIIGLWGVVIAT 551

RESULT 15
 O98SGO PRELIMINARY; PRT; 693 AA.
 ID O98SGO

AC O98SGO;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE BETA-AMYLOID PRECURSOR PROTEIN A.
 GN APP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCBL_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA van den Hark W.H.;
 RL Thesis (2001), Department of Biological Sciences,
 RL University of Nijmegen, Nijmegen, Netherlands.
 DR EMBL; AJ298150; CAC37193.1; -
 DR HSSP; P05067; 1H23.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS; PRO0203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Signal.
 FT SIGNAL 1 18
 FT SIGNAL 18 18
 SQ SEQUENCE 693 AA; 78568 MW; CAFIDF65C1AB653 CRC64;

Query Match 91.4%; Score 203; DB 13; Length 693;
 Best Local Similarity 88.4%; Pred. No. 4.1e-18;
 Matches 38; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 DAEFRHDSGEVHHOKLVFEADVGSNKGAIIIGLWGVVIAT 43
 DB 595 DSEYRHDTAEVHHOKLVFEADVGSNKGAIIIGLWGVVIAT 637

Search completed: October 31, 2002, 10:14:35
 Job time : 4.69742 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:50 ; Search time 3.01476 Seconds
(without alignments)
1584.263 Million cell updates/sec

Title: US-09-785-215-2_COPY_672_714

Perfect score: 222

Sequence: 1 DAFFRHDSGEVHHKLVFF.....VGSNKGAIIGLMGVVIAT 43

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_032802.*

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- 2: /SIDSI/gcgdata/geneseq/genesqp-emb1/AA1981.DAT.*
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- 19: /SIDSI/gcgdata/geneseq/genesqp-emb1/AA1998.DAT.*
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- 21: /SIDSI/gcgdata/geneseq/genesqp-emb1/AA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/genesqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	222	100.0	43	15	AA54759
2	222	100.0	43	15	AA60367
3	222	100.0	43	15	AA61328
4	222	100.0	43	16	AA64165
5	222	100.0	43	17	AA65673
6	222	100.0	43	18	AA69371
7	222	100.0	43	19	AA71758
8	222	100.0	43	19	AA71378
9	222	100.0	43	19	AA51316
10	222	100.0	43	19	AA40129
11	222	100.0	43	20	AA42955

12	222	100.0	43	20	AA89362	Beta-amyloid pepti
13	222	100.0	43	21	AA27020	Beta-amyloid pepti
14	222	100.0	43	21	AA15372	Human beta-amyloid
15	222	100.0	43	21	AA21216	Beta-amyloid pepti
16	222	100.0	43	21	AA88390	Beta-amyloid pepti
17	222	100.0	43	21	AA56102	Natural beta amylo
18	222	100.0	43	22	AA678791	Human beta amyloid
19	222	100.0	43	22	AAE12508	Beta-amyloid pepti
20	222	100.0	43	22	AA88428	Partial sequence o
21	222	100.0	43	22	AA89896	Beta-amyloid pepti
22	222	100.0	43	22	AA81193	Beta-amyloid pepti
23	222	100.0	43	22	AA89178	Amyloid beta-prote
24	222	100.0	43	22	AA891811	Amyloid beta-prote
25	222	100.0	43	22	AA847108	Biotinylated beta-
26	222	100.0	43	22	AA848344	Beta-amyloid pepti
27	222	100.0	45	16	AA64169	Variant beta amylo
28	222	100.0	47	20	AA81475	Synthetic amyloid
29	222	100.0	48	22	AA837523	Variant beta amylo
30	222	100.0	52	16	AA64166	Amyloid precursor
31	222	100.0	52	20	AA81476	Synthetic amyloid
32	222	100.0	53	15	AA55695	Sequence of uniden
33	222	100.0	53	16	AA64168	Variant beta amylo
34	222	100.0	54	21	AA832126	Amyloid-beta precu
35	222	100.0	55	22	AA811482	Human APP peptide
36	222	100.0	57	21	AA810910	Human amyloid prec
37	222	100.0	59	17	AAW05375	Amyloid precursor
38	222	100.0	59	19	AAW70863	Beta-amyloid precu
39	222	100.0	59	22	AA88425	Partial sequence o
40	222	100.0	60	21	AA64747	Beta-amyloid precu
41	222	100.0	63	19	AAW44747	APP-REP 751 BAP pe
42	222	100.0	63	19	AAW42976	Beta-amyloid pepti
43	222	100.0	70	22	AAE09373	Human wild-type AP
44	222	100.0	70	22	AAE09374	Human APP695 Swedi
45	222	100.0	70	22	AAE09375	Human truncated AP

ALIGNMENTS

RESULT 1
ID AARS4759 standard; peptide; 43 AA.
XX AARS4759;
AC AARS4759; (first entry)
DT 30-NOV-1994
XX
XX Beta amyloid peptide.
DE
DE Beta amyloid peptide.
KW Beta amyloid peptide; amyloid plaques; Alzheimer's disease; lesion;
KW brain; senility; dementia; detection; diagnosis.
XX
XX Homo sapiens.
OS
XX
XX W09410569-A.
PN
XX
PD 11-MAY-1994.
XX
XX 01-SEP-1993; 93WO-US08264.
XX
XX 26-OCT-1992; 92US-0965972.
XX
XX (SCHE/) SCHEHN D B.
XX (SCHL/) SCHLOSSMACHER M G.
XX (SELK/) SELKOE D.
XX
XX Schenk DB, Schlossmacher MG, Selkoe DJ, Seubert PA;
XX Vligo-pelfrey; C.
XX WPI; 1994-167654/20.
XX
XX Detecting soluble beta-amyloid peptide concns. e.g. for
XX diagnosing and assessing progression of Alzheimer's disease - by

PT exposing cultured cells to test cpd. to determine effect of cpd.
 PT on produced soluble beta-amyloid peptide
 XX
 PS Disclosure; Page 10; 55pp; English.
 CC Beta amyloid peptide is the principal chemical constituent of
 CC amyloid plaques, lesions found on the brains of Alzheimer's disease
 CC patients. The ability to detect beta amyloid peptide in fluid
 CC samples provides a means of diagnosing Alzheimer's disease.
 XX
 SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 15; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 2

AA60367
 ID AAR60367 standard; peptide; 43 AA.

AC AAR60367;

DT 15-MAR-1995 (first entry)

DE Beta-amyloid (1-43).

XX Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
 XX anti-beta-amyloid antibody; diagnosis.

OS Homo sapiens.

PN WO9417197-A.

PD 04-AUG-1994.

PF 24-JAN-1994; 94WO-JP00089.

PR 25-JAN-1993; 93JP-0010132.

PR 05-FEB-1993; 93JP-0019035.

PR 16-NOV-1993; 93JP-0286985.

PR 28-DEC-1993; 93JP-0334773.

(TAKE) TAKEDA CHEM IND LTD.

XX Kitada C, Odaka A, Suzuki N;

DR WPI; 1994-264110/32.

PT Antibodies recognising specific parts of beta-amyloid - can be
 PT used for diagnosis of diseases implicating beta-amyloid, such as
 PT Alzheimer's disease

PS Disclosure; Page 83; 116pp; Japanese.

CC Antibodies which recognise specific subfragments of the beta-amyloid
 CC protein are claimed. Specifically, the antibodies (which are pref.
 CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
 CC portion of beta-amyloid or they recognise residues 25-35 or 35-43
 CC from the C-terminal portion. The antibodies are useful for assaying
 CC beta-amyloid and its derivatives for diagnosis of Alzheimer's
 CC disease.

XX Sequence 43 AA;

Query Match 100.0%; Score 222; DB 15; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

Db AAR61328
 ID AAR61328 standard; Protein; 43 AA.

AC AAR61328;

DT 21-APR-1995 (first entry)

DE Amyloid beta-protein, ABP.

XX Amyloid beta-protein; ABP; Tau-protein kinase I enzyme; TRK-I;
 XX Alzheimer's disease.

OS Synthetic.

PN EP616032-A.

PD 21-SEP-1994.

PF 01-MAR-1994; 94EP-0103057.

PR 02-MAR-1993; 93JP-0041160.

PR 22-MAR-1993; 93JP-0085143.

PR 02-AUG-1993; 93JP-0191246.

(TAKA/) TAKASHIMA A.

PA (MITU) MITSUBISHI KASEI CORP.

PI Hoshino T, Imahori K, Saito K, Sato S, Shiratsuchi A;

DR Takashima A;

DR WPI; 1994-287181/36.

PT Newly isolated tau-protein kinase I enzyme - with specificity for
 PT tau-protein providing means for prevention and treatment of
 PT Alzheimer's disease

PS Example 1; Page 22; 30pp; English.

CC Amyloid beta-protein (ABP) is the main component of senile plaques
 CC in Alzheimer's disease. ABP was used to demonstrate the protective
 CC properties of anti-sense TRK-I oligonucleotides (AA067461 and AA067462)
 CC on hippocampus cells dosed with ABP.

XX Sequence 43 AA;

Query Match 100.0%; Score 222; DB 15; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIAT 43
 1 DAEFRHDSGYEVHOKLVFFAEDVGSNKGAIIGLMVGVVIAT 43

Db AAR64165
 ID AAR64165 standard; peptide; 43 AA.

AC AAR64165;

DT 02-AUG-1995 (first entry)

DE Beta amyloid protein.

XX beta amyloid protein; mutant; variant; detection; amyloid deposition;
 XX diagnosis; amyloidosis associated disease; Alzheimer's disease;
 XX Down's syndrome.

XX OS Synthetic.
XX PN WO9428412-A.
XX PD 08-DEC-1994.
XX PF 27-MAY-1994; 94WO-US05809.
XX PR 28-MAY-1993; 93US-0069010.
XX PA (MIRI-) MIRIAM HOSPITAL.
XX PI Majocha RE, Marotta CA;
XX DR WPI; 1995-023013/03.
XX PT

Amyloid binding composition comprising labelled amyloid protein and carrier - useful for in vivo imaging of amyloid deposits, for diagnosing Alzheimer's disease and Down's Syndrome.

475 Claim 5; Page 42; 58pp; English.

XX CC AAR64165 shows the amino acid sequence of the beta amyloid protein. The
XX CC protein binds amyloid and is useful for in vivo imaging of amyloid
XX CC deposits and hence diagnosis of an amyloidosis-associated disease, such
XX CC as Alzheimer's disease or Down's syndrome. AAR64165-69 show specific
XX CC variants generated from this generic sequence with addition amino acids.
XX SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 16; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFEADVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHOKLVFEADVGSNKGAIIGLMVGVVIAT 43

RESULT 5
AAR95673
ID AAR95673 standard; Peptide; 43 AA.
XX AC AAR95673;
XX PD 24-FEB-1997 (first entry)
XX PF A-beta protein (43 amino acid version).
XX PR A-beta protein; beta-amyloid precursor protein; APP; Alzheimer's disease;
XX KM diagnosis; monitor; amyloid plaque; senile.
XX OS Homo sapiens.
XX PN WO9615452-A1.
XX PD 23-MAY-1996.
XX PF 13-NOV-1995; 95WO-US14659.
XX PR 07-APR-1995; 95US-0419008.
XX PR 14-NOV-1994; 94US-0339141.
XX PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX PI Barbour R, Schenk DB, Seubert PA, Vigo-pelfrey C;
XX DR WPI; 1996-260003/26.
XX PT Diagnosis and monitoring of Alzheimer's disease - by detecting
XX PT abnormally low concentration of A-beta peptide extending beyond
XX PT amino acid 41 in cerebrospinal fluid

XX PS Disclosure; Page 16; 57pp; English.
XX CC The "amyloid-beta peptide" or A-beta is an approx. 4.2 kD protein which,
XX CC in the brains of Alzheimer's disease, Down's Syndrome, HCHWA-D and some
XX CC normal aged subjects, forms the subunit of amyloid filaments comprising
XX CC the senile (amyloid) plaques and the amyloid deposits in small cerebral
XX CC and meningeal blood vessels. A-beta is an approx. 39-43 amino acid
XX CC fragment of a large membrane-spanning glycoprotein, referred to as the
XX CC beta-amyloid precursor protein (APP), encoded by a gene on the long arm
XX CC of human chromosome 21. Detecting the amt. of A-beta is useful in
XX CC diagnosis and monitoring of Alzheimer's disease, when taken together
XX CC with other clinical symptoms. The present sequence is a 43 amino acid
XX CC version of A-beta.
XX SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 17; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAEFRHDSGYEVHHOKLVFEADVGSNKGAIIGLMVGVVIAT 43
DB 1 DAEFRHDSGYEVHHOKLVFEADVGSNKGAIIGLMVGVVIAT 43

RESULT 6
AAW93371
ID AAW93371 standard; Protein; 43 AA.
XX AC AAW93371;
XX PD 28-MAY-1999 (first entry)
XX PF Human beta-amyloid polypeptide.
XX PR Cathepsin Y; human; beta-amyloid peptide; BAP; secretion; inhibitor;
XX KM protease; carboxypeptidase; aliphatic C-terminal amino acid; diagnostic;
XX KM glycoprotein; cerebral deposition; pathogenesis; Alzheimer's disease;
XX KM detection; amyloid plaque; angiodopathy; brain; Trisomy 21; amyloidosis;
XX KM Down's syndrome; hereditary cerebral haemorrhage.
XX OS Homo sapiens.
XX PN WO9639194-A1.
XX PD 12-DEC-1996.
XX PF 26-APR-1996; 96WO-US06211.
XX PR 06-JUN-1995; 95US-0469362.
XX PR 06-JUN-1995; 95US-0467607.
XX PR 02-MAY-1997; 97US-0850392.
XX PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX PA (ANDE-) ANDERSON J.
XX PA (CHRY/) CHRYSLER S.
XX PA (MCCO/) MCCONLOGUE L.
XX PA (SINH/) SINHA S.
XX PA (TATS/) TATSUNO G.
XX PA (TUNG/) TUNG JS.
XX PI Anderson J, Chrysler S, McConlogue L, Semko CMF;
XX PI Sinha S, Tatsuno G, Tung JS;
XX DR WPI; 1997-042872/04.
XX PT Acylamino and acyl-peptido-amino alcohol and aldehyde derivs. -
XX PT inhibit beta-amyloid peptide prodn. in cells, use in Alzheimer's
XX PT disease, also prepn. of cathepsin Y and nucleic acid encoding for
XX PT it.
XX PS Disclosure; Page 11; 90pp; English.

XX This invention describes the inhibition of beta-amyloid peptide
 CC production in cells is effected by administration of an acylamino or
 CC acylpeptidomino alcohol or aldehyde derivative of formula
 CC R1(X)m-Y-NR-CHN2-[CONR10-CHN3]n-R4 where R and R10 = H or 1-6C alkyl;
 CC or R and R2 together, and/or R10 and R3 together complete a 4-10C ring
 CC structure; R1 = (a) 1-4C alkyl substd. by 1-5 substituents chosen from 6-10C
 CC aryl (opt. substd. by 1-3 of 1-6C alkyl, 1-6C alkoxy, 6-10C aryl, 6-10C
 CC arylalkoxy, OH, cyano, halo and amino), 3-8C cycloalkyl or Het, in which the
 CC substd. alkyl gp. is opt. further substd. by 1 or 2 of OH; (b) 2-4C
 CC alkanyl substd. by 1-4 substituents as for 1-4C alkyl above; (c) 6-10C aryl
 CC (opt. substd. by 1-3 substituents as for alkyl above), (d) fluorenyl or (e)
 CC Het; Het = 3-14C heterocyclyl contg. 1-3 N, 0 or S heteroatoms; R2 and R3
 CC = D- or L- amino acid side chains of at least 2C atoms, excluding prolyl
 CC side chain; R4 = COCH-N2, CH2OH, C=NOH or COR5; R5 = H, 1-6C alkyl (opt.
 CC contg. 1 or 2 halogen atoms), 1-6C alkoxy, NR6R7 or N(Me)OMe; R6 and R7
 CC = H or 1-6C alkyl; X = O, NR9 or S; R9 = H, 1-6C alkyl or 6-10C aryl; Y =
 CC CO or CS; m = 0 or 1; and n = 0-2; provided that (i) when R1 =
 CC 1-naphthyl, R2 = CHMe2 (L-isomer), R3 = benzyl (L-isomer), Y = CO, m =
 CC 0 and n = 1, then R4 (sic) is not N(Me)OMe; (ii) when R1 = CHPh2, R2 =
 CC p-benzoyloxybenzyl (L-isomer), Y = CO, and m = n = 0, then R4 (sic) is
 CC not N(Me)OMe; and (iii) when R1 = PhCH-CPh, Y = CO, R2 = benzyl
 CC (L-isomer) and m = n = 0, then R4 (sic) is not N(Me)OMe. Cathepsin Y is
 CC a 31 kD carboxypeptidase with particular activity for aliphatic
 CC C-terminal amino acids. It is involved in the generation of beta-amyloid
 CC protein (BAP) from its precursor glycoprotein. Cerebral deposition of BAP
 CC plays a key role in pathogenesis of Alzheimer's disease (AD), and its
 CC detection can precede openly apparent symptoms of AD by years or more.

CC Amyloid plaques and angiopathy are also present in the brain in those
 CC having Trisomy 21 (Down's syndrome) and hereditary cerebral haemorrhage
 CC with amyloidosis of Dutch type (HCHWA-D). The inhibitors are of use in
 CC inhibiting such plaque deposition and in treating AD. The cathepsin Y can
 CC be used, by virtue of its carboxypeptidase activity, in screening for BAP
 CC prodn. inhibitors, and, more widely, as a general C-terminal protease in
 CC a variety of chemical and biological systems. Conversely, assay of
 CC cathepsin Y in body fluid can be used diagnostically to evaluate the
 CC future risk of developing AD. The nucleic acid can be used to probe
 CC specifically for presence of cathepsin Y RNA or DNA in tissues or cloned
 CC libraries. It can also be used for expression of recombinant cathepsin Y,
 CC by transfection of a host cell.

SO Sequence 43 AA;

Query Match 100.0%; Score 222; DB 18; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 DAEFRHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVYAT 43
 ||||||||||||||||||||||||||||||||||||||||
 1 DAEFRHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVYAT 43

RESULT 7

AA17758
 ID AAY17758 standard; peptide; 43 AA.

AC AAY17758;

DT 10-AUG-1999 (first entry)

DE Beta-amyloid peptide.

KW Beta-amyloid peptide; beta-amyloid precursor protein; APP;
 membrane spanning glycoprotein; Alzheimer's disease.

OS Homo sapiens.

PN WO9822493-A2.

PD 28-MAY-1998.

PF 20-NOV-1997; 97WO-US18704.

XX

PR 22-NOV-1996; 96US-0755334.

PA (ATHE-) ATHENA NEUROSCIENCES INC.

PA (ELIL) LILLY & CO ELI.

PI Audia JE, Folmer BK, John V, Latimer LH, Nissen JS;

PI Porter WJ, Thorsett ED, Wu J;

DR WPI; 1998-322359/28.

PT New and known aryl or hetero-aryl amino acid derivatives - useful
 PT for inhibiting beta-amyloid peptide release and/or its synthesis and
 PT treating Alzheimer's disease

XX disclosing; page 19; 131pp; English.

XX The present invention describes a composition comprising an inert carrier
 CC and an N-(aryl or heteroaryl) amino acid derivative e.g.
 CC N-[N-(3,4-dichlorophenyl)alaninyl] valine methyl ester. The composition
 CC can be used for inhibiting beta-amyloid peptide release and/or its
 CC synthesis in a cell, for preventing the onset of Alzheimer's disease
 CC and for treating Alzheimer's disease in order to inhibit further
 CC deterioration. The dosage is 0.1-500 mg/kg/day orally, rectally,
 CC transdermally, subcutaneously or intravenously. The present sequence
 CC represents the beta-amyloid peptide.

SO Sequence 43 AA;

Query Match 100.0%; Score 222; DB 19; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVYAT 43
 ||||||||||||||||||||||||||||||||||||||||
 Db 1 DAEFRHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVYAT 43

RESULT 8

AAW1378
 ID AAW1378 standard; peptide; 43 AA.

AC AAW1378;

DT 02-DEC-1998 (first entry)

DE Beta-amyloid precursor protein epitope.

KW Beta amyloid precursor protein; eukaryotic cell line;
 KW exogenous gene construction; identification; quantification;
 KW inhibitor; beta-amyloid processing; treatment; Alzheimer's disease;
 KW brain trauma; Downs syndrome.

OS Homo sapiens.

PN WO9837215-A1.

PD 27-AUG-1998.

PF 03-FEB-1998; 98WO-US01899.

PR 31-JUL-1997; 97US-0904296.

PR 24-FEB-1997; 97US-0804971.

PR 02-APR-1997; 97US-0825737.

PA (HMRI) HOECHST MARION ROUSSEL INC.

PA (SCIO-) SCTIOS INC.

PI Cordell B, Huggins J, Mischak RP, Pruss R, Rautmann G;

PI Scardina JW;

DR WPI; 1998-495368/42.

PT New eukaryotic cell lines - containing a gene construct containing a

PT beta-amyloid precursor protein encoding sequence, used for
 PT identifying inhibitors of beta-amyloid processing
 XX
 PS Disclosure: Fig 5; 82pp; English.
 CC
 CC The present sequence represents an epitope derived from a beta amyloid
 CC precursor protein, and recognised by antibodies BA1, 108.1, 1702.1,
 CC and 1101.1. The specification describes an eukaryotic cell line
 CC having exogenous gene construction comprising a cytomagalovirus (CMV)
 CC promoter, a strong ribosome binding site (RBS), a beta-amyloid
 CC precursor protein (BAP) nucleic acid sequence, a selectable marker,
 CC and a poly-adenylation signal. The products can be used for identifying
 CC or quantifying beta-amyloid protein and for identifying inhibitors of
 CC beta-amyloid processing. They can be used to develop products for
 CC treating amyloidosis, e.g. Alzheimer's disease, brain trauma or Downs
 CC syndrome.
 XX
 SQ Sequence 43 AA:
 Query Match 100.0%; Score 222; DB 19; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DAEFRHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVVIAT 43
 1 DAEFRHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVVIAT 43
 DB 1 DAEFRHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVVIAT 43
 RESULT 9
 AAM51316
 ID AAM51316 standard; peptide: 43 AA.
 XX
 AC AAM51316;
 XX
 DT 14-AUG-1998 (first entry)
 XX
 DE Natural beta-amyloid peptide fragment.
 XX
 KW Natural beta-amyloid peptide; aggregation; D-amino acid;
 KW Alzheimer's disease; beta-amyloidosis.
 XX
 OS Homo sapiens.
 XX
 PN WO9808868-A1.
 PD 05-MAR-1998.
 XX
 PR 27-AUG-1997; 97WO-US15166.
 XX
 PR 21-JUL-1997; 97US-0897342.
 PR 27-AUG-1996; 96US-0703675.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 PI Arico-muendel CG, Chin J, Findeis MA, Gelfer ML;
 PI Hayward NJ, Kelley M, Komar-panicucci S, Lee J, Molineaux S;
 PI Musso G, Phillips K, Signer ER, Wakefield J;
 XX
 DR WPI; 1998-216936/19.
 XX
 PT Peptide compounds which are preferably based on beta-amyloid
 PT peptide(s) - are useful in treatment of disorders related to
 PT beta-amyloidosis, especially Alzheimer's disease
 XX
 PS Disclosure: Page 8; 92pp; English.
 CC
 CC The invention relates to peptides that modulate natural beta-amyloid
 CC peptide aggregation. The modulators of the invention comprise a peptide
 CC preferably based on a beta-amyloid peptide, that is comprised entirely
 CC of D-amino acids. Preferably the peptide comprises 3-5 D-amino acid
 CC residues and includes at least two D-amino acid residues independently
 CC selected from the group consisting of D-leucine, D-phenylalanine and
 CC D-valine. Preferred amino-terminal modifying groups include cyclic,

CC heterocyclic, polycyclic and branched alkyl groups. Preferred
 CC carboxy-terminal modifying groups include an amide group, an alkyl amide
 CC group, an aryl amide group or a hydroxy group. The peptides may be used
 CC to treat disorders associated with beta-amyloidosis, especially
 CC Alzheimer's disease. They may also be used in methods for detecting the
 CC presence of beta-amyloid peptides in biological samples. The present
 CC sequence represents the 43 amino acid long form of natural beta-amyloid
 CC peptide.
 XX
 SQ Sequence 43 AA:
 Query Match 100.0%; Score 222; DB 19; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DAEFRHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVVIAT 43
 1 DAEFRHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVVIAT 43
 DB 1 DAEFRHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVVIAT 43
 RESULT 10
 AAM40129
 ID AAM40129 standard; peptide: 43 AA.
 XX
 AC AAM40129;
 XX
 DT 03-JUN-1998 (first entry)
 XX
 DE Human amyloid-beta peptide.
 XX
 KW Amyloid-beta peptide; A-beta; senile plaque; angiopathy;
 KW brain; membrane-spanning glycoprotein; beta-amyloid precursor protein;
 KW APP; chromosome 21; human; Alzheimer's disease; AD; amyloid filament;
 KW treatment; disease; Down's syndrome; hereditary cerebral haemorrhage.
 XX
 OS Homo sapiens.
 XX
 PN WO9748983-A1.
 PD 24-DEC-1997.
 XX
 PR 18-JUN-1997; 97WO-US10601.
 XX
 PR 18-JUN-1996; 96US-0665649.
 XX
 PA (ATHE-) ATHENA NEUROSCIENCES INC.
 PA (BGHM-) BRIGHAM & WOMEN'S HOSPITAL.
 XX
 PI Citron M, Schenk D, Selkoe DJ, Seubert PA;
 XX
 DR WPI; 1998-063287/06.
 XX
 PT Identifying compounds that alter cellular production of amyloid-beta
 PT 42 fragment - in vitro or in transgenic animal models, potentially
 PT useful for treatment of Alzheimer's and other amyloid deposition
 PT diseases
 XX
 PS Disclosure: Page 15; 86pp; English.
 CC
 CC This sequence represents a human amyloid-beta peptide (A-beta) which is a
 CC fragment of the of a large membrane-spanning glycoprotein referred to as
 CC the beta-amyloid precursor protein (APP) encoded by a gene on the long
 CC arm of chromosome 21. This peptide is also known as the beta-AP peptide
 CC and forms the subunit of the amyloid filaments comprising senile
 CC (amyloid) plaques and the amyloid deposits in small cerebral and
 CC meningeal blood vessels (amyloid angiopathy). The A-beta peptide can be
 CC a 39-43 amino acid fragment. This invention provides methods of screening
 CC compounds for their ability to alter the production of the A-beta
 CC peptide, which is composed of >41 amino acids, alone, or in combination
 CC with the A-beta peptide composed of 40 amino acids or less. Such agents
 CC that reduce the production of the A-beta peptide are potentially useful
 CC for treatment of Alzheimer's Disease or other diseases involving amyloid
 CC deposition such as Down's syndrome, hereditary cerebral haemorrhage with

CC amyloidosis of Dutch type and advanced aging of the brain.

XX
SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 19; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-25;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 11

AA42955

ID AAY42955 standard; protein; 43 AA.

XX AAY42955;

02-JAN-2000 (first entry)

Beta-amyloid precursor protein.

Beta-amyloid precursor protein; APP; release inhibition;

Alzheimer's disease.

Homo sapiens.

XX US5965614-A.

XX 12-OCT-1999.

XX 21-NOV-1997; 97US-0975977.

XX 22-NOV-1996; 96US-0104593.

(ATHE-) ATHENA NEUROSCIENCES INC.

Folmer BK, Audia JE, Latimer LH, Nissen JS, Reel JK, Thorsett ED;

Whitesitt CA, John V.

WPI; 1999-579933/49.

Process for inhibiting beta-amyloid peptide cellular release and/or
PT synthesis comprising administration of N-(aryl/heteroaryl) amino acid
PT ester derivatives, useful for treatment and prevention of Alzheimer's
disease -

disclosure; Column 49; 29pp; English.

New chemical compounds are disclosed which inhibit the cellular

release and/or synthesis of beta-amyloid peptide (the present sequence).

The compounds are N-(aryl or heteroaryl) amino acid ester derivatives, of

which N-(3,4-dichlorophenyl)alanine ethyl ester is a specific example.

These compounds can be used for the treatment and prevention of

Alzheimer's disease.

XX Sequence 43 AA;

Query Match 100.0%; Score 222; DB 20; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-25;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 12

AAW89362

ID AAW89362 standard; peptide; 43 AA.

XX AAW89362;

XX 02-MAR-1999 (first entry)

Beta-amyloid peptide derivative A-beta-1-43.

Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;

aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;

familial amyloid polyneuropathy; bovine spongiform encephalopathy;

Creutzfeldt-Jakob disease; BAP.

Homo sapiens.

Synthetic.

US5854204-A.

29-DEC-1998.

14-MAR-1996; 96US-0612785.

14-MAR-1996; 96US-0612785.

14-MAR-1996; 96US-0612785.

14-MAR-1996; 96US-0612785.

14-MAR-1996; 96US-0612785.

14-MAR-1996; 96US-0612785.

WPI; 1999-094964/08.

New peptide(s) derived from beta-amyloid peptide that inhibit
PT amyloid aggregation - and neurotoxicity, specifically for treatment
PT and prevention of Alzheimer's disease

Example 1; Column 46; 52pp; English.

The present invention describes beta-amyloid peptide (BAP) derivatives.
CC The BAP derivatives inhibit aggregation of amyloidogenic proteins and
CC peptides, specifically BAP, and their neurotoxicity, so are useful for
CC treating and preventing any disease involving amyloidosis, specifically
CC Alzheimer's disease but also Down's syndrome, familial amyloid
CC polyneuropathy or cardiomyopathy, bovine spongiform encephalopathy and
CC Creutzfeldt-Jakob disease. The BAP derivatives are also used to diagnose
CC these diseases, in vitro or in vivo, by detecting binding of BAP to
CC labelled BAP derivatives. Some BAP derivatives inhibit BAP aggregation
CC even when BAP is present in molar excess. The present sequence
CC represents a BAP derivative.

XX Sequence 43 AA;

Query Match 100.0%; Score 222; DB 20; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.6e-25;

Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

DB 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMVGVVIAT 43

RESULT 13

AAW27020

ID AAW27020 standard; protein; 43 AA.

XX AAW27020;

02-FEB-2001 (first entry)

Beta-amyloid peptide.

Beta-amyloid peptide; nootropic; neuroprotective; Alzheimer's disease.

Dd	1	MLNDGYMLPCGIDKRGVIEFCCSLAEBSDSVDAAEEDSDVMWGADTDYADGGD	60
Qy	224	KVVEVAEEEAEEVAEEEADEDDDEDDDEVEEAEEBEPEATEERTSIATTTTTTESV	28
Dd	61	KVVEVAEEEAADVEEAADDDDEDDDEVEEAEEBEPEATEERTSIATTTTTTESV	12
Qy	284	EEVREYCSQATGTGCRAMISRWTFEDVTEGKCAFETYGGCGNRNFDTEECMAVCS	34
Dd	121	EEVREYCSQATGTGCRAMISRWTFEDVTEGKCAFETYGGCGNRNFDTEECMAVCS	18
Qy	344	AMSOSLKTTOEPLADPKLTPTAASRPDAVDKYLEPGEENHAHFOAKERLAKHR	40
Dd	181	VSTOSLKTTSPLPDPDPKLTPTAASRPDAVDKYLEPGEENHAHFOAKERLAKHR	24
Qy	404	ERMOSVREWEAEERQAKMLPRADKKAIVIOHFOEKVESTLEQAEANEHQQLVETHMARVE	46
Dd	241	ERMOSVREWEAEERQAKMLPRADKKAIVIOHFOEKVESTLEQAEANEHQQLVETHMARVE	30
Qy	464	MLNDRRLALENTITLQAVPRPRPHVFMMLKKYVRAEQKDRQHTLKHFEHVMADPKKA	52
Dd	301	MLNDRRLALENTITLQAVPRPRPHVFMMLKKYVRAEQKDRQHTLKHFEHVMADPKKA	36
Qy	524	AQISQVMTLRTVYERMMOSLSLLYNPVAAVEEIODVDLQKQONTSDVLANMISE	58
Dd	361	AQISQVMTLRTVYERMMOSLSLLYNPVAAVEEIODVDLQKQONTSDVLANMISE	42
Qy	584	PRISYGDALMPRLTETKTTVELLPVNGEFSLDDIQPHNSFGADSVANTENEVEPYDAR	64
Dd	421	PRISYGDALMPRLTETKTTVELLPVNGEFSLDDIQPHNSFGADSVANTENEVEPYDAR	48
Qy	644	PADRGITTPSGGLTNITBELSEYKDDAEFRHDSGTEVNHOKLVYFAEDVGSNKGAT	70
Dd	481	PADRGITTPSGGLTNITBELSEYKDDAEFRHDSGTEVNHOKLVYFAEDVGSNKGAT	54
Qy	704	GLMWGVIAITVITVLWMLKKQOTSIHHGVAEVDAVATPEERHLSKMOONGENPTYK	76
Dd	541	GLMWGVIAITVITVLWMLKKQOTSIHHGVAEVDAVATPEERHLSKMOONGENPTYK	60
Qy	764	FEEDOMN 770	
Dd	601	FEEDOMN 607	
RESULT 11			
ID	057394	PRELIMINARY:	PRT: 699 AA.
AC	057394:		
DT	01-JUN-1998 (TEMBLrel. 06, Created)		
DT	01-JUN-1998 (TEMBLrel. 06, Last sequence update)		
DT	01-DEC-2001 (TEMBLrel. 19, Last annotation update)		
DE	EL AMYLOID PRECURSOR PROTEIN 699.		
GN	EL APP699.		
OS	Nelk japonica (Electric ray).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;		
OC	Elasmobranchii; Squala; Hyposquala; Pristiogaster; Batoidae.		
OC	Torpediniformes; Narcinoidae; Narkidae; Narkae.		
OX	NCBI_TaxID=62965;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Electric LOBE;		
EX	MEDLINE=98129705; PubMed=9461486;		
RA	Iijima K., Lee D.-S., Okutsu J., Tomita S., Hirashima N., Kirino Y.,		
RT	Suzuki T.;		
RT	"cDNA isolation of Alzheimer's amyloid precursor protein from		
RT	cholinergic nerve terminals of the electric organ of the electric		
RT	ray.";		
RL	Biochem. J. 330:29-33(1998).		
DR	EMBL; AB003544; BAA24230.1; -.		
DR	HSSP; P05067; IH23.		
DR	InterPro; IPR001868; A4_APP.		
DR	Pfam; PF02177; A4_EXTRA.1.		
DR	PRINTS; PRO0203; AMYJOIA4.		
DR	SMART; SM00006; A4_EXTRA.1.		

DR PROSITE; PS00319; A4-EXTRA; 1.
DR PROSITE; PS00320; A4-INTRA; 1.
SQ SEQUENCE 699 AA; 78879 MW; 952915C309D50E5C CRC64;

Query Match 71.8%; Score 2914; DB 13; Length 699;
Best Local Similarity 72.9%; Pred. No. 9.3e-174;
Matches 568; Conservative 59; Mismatches 58; Indels 94; Gaps 9;

```

OY 2 LFG-LALLLLAAMTA-----RALEVPDGNAGLL-AEPOTAMFCGRNMNMNONGKW 52
DB 5 LPRGLGMLLAALAAALVLAFLCLALEVPPDGGAGLLAEPQJAMFCGRNMNMNONGKW 64
OY 53 DSDPSGTCTIDTKEGIILOYCOEYVPELOITNVVEANOPVTIONMCKRGKCKTHPHFV 112
DB 65 VSDPSGTCTIDTKEGIILOYCOEYVPELOITNVVEANOPVTIONMCKRGKCKTHPHFV 124
OY 113 IPRCLVGEFVSADALLVPDKCFLEQERNDVCEYLHMHHTVAKETCSKSTYLAHYGML 172
DB 125 VPRCLVGEFVSADALLVPDKCFLEQERNDVCEYLHMHHTVAKETCSKSTYLAHYGML 184
OY 173 PCGIDKFRGVEFVCCPLAEEESDNDVSADAEEDSDVMWGADTDYADGSEDKVVEAEE 232
DB 185 PCGIDKFRGVEFVCCPLAEEESDNDVSADAEEDSDVMWGADTDYADGSEDKVVEAEE 238
OY 233 EVAEEVEEADDEDEDEDEDEVEE-ABEYVEATERTSIAITTTTTEVEEYVREV 291
DB 239 KPIEEEEDESDIDDEDDDDDEVEDEYEDYEDPTHTTS---STTTTTEAEEVVR--- 292
OY 292 SEQATGCRAMISRWYEDVTEGKCAPEFYGGCGGNRNNEFTEEYCAVCGSAMQSILK 351
DB 293 ----- 292
OY 352 TTEPLANDPYLPTTAATSTPDADVDTLETGDENEHAHFOKAKERLEKHKRERSOYMR 411
DB 293 -----VPTTAATSTPDADVDTLETGDENEHAHFOKAKERLEKHKRERSOYMR 411
OY 412 EWEAEERQAKNLPRKADKAVIOHFOEKVESLEQEAANEQOOLVETHMAVEMALNDRRL 471
DB 341 EWEAEERQAKNLPRKADKAVIOHFOEKVESLEQEAANEQOOLVETHMAVEMALNDRRL 400
OY 412 ALENTITLQAVPRPRHVNMLKKYRAEOKRQHTLKHFNHVMNVPKRAQQRQVM 531
DB 401 ALENTITLQAVPRPRHVNMLKKYRAEOKRQHTLKHFNHVMNVPKRAQQRQVM 460
OY 412 ALENTITLQAVPRPRHVNMLKKYRAEOKRQHTLKHFNHVMNVPKRAQQRQVM 531
DB 401 ALENTITLQAVPRPRHVNMLKKYRAEOKRQHTLKHFNHVMNVPKRAQQRQVM 460
OY 532 THIRYIYRMANOSLVLNVPAVAEIODEVDLQEQNSDVLIANNISEPRISYND 591
DB 461 THIRYIYRMANOSLVLNVPAVAEIODEVDLQEQNSDVLIANNISEPRISYND 520
OY 532 ALMPSLETCTVELLPVNGEFLDLOPWHISFGADSVPAANTENEPVDAHPADRGLT 651
DB 521 ALMPSLETCTVELLPVNGEFLDLOPWHISFGADSVPAANTENEPVDAHPADRGLT 580
OY 652 TRPGGLNITTEISEYKMADEFRHDSGYEHOKLVFPFADVGSNKGATITGLWGVV 711
DB 561 TRPGGLNITTEISEYKMADEFRHDSGYEHOKLVFPFADVGSNKGATITGLWGVV 640
OY 712 IATVIVITLMLKKQYTSIHGVEVDAAVTPPEERHLSKMOQNSYENPTYKFEFOMON 770
DB 641 IATVIVITLMLKKQYTSIHGVEVDAAVTPPEERHLSKMOQNSYENPTYKFEFOMON 699

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RESULT 12
013764 PRELIMINARY: PRT: 547 AA.

AC 013764:
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE AMYLOID-BETA PROTEIN.
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikai S., Sasaki H., Doh-ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor gene
[published erratum appears in Gene 1991 Jun 30;102(2):291-2].";
RL Gene 87:257-263(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA Yoshida K., Izumi R., Oishi N., Sakaki Y.;
RL Submitted (SEP-1990) to the EMBL/GenBank/DBJ databases.

DR EMBL; M34875; AAB59501.1; JOINED.
DR EMBL; M34862; AAB59501.1; JOINED.
DR EMBL; M34863; AAB59501.1; JOINED.
DR EMBL; M34864; AAB59501.1; JOINED.
DR EMBL; M34865; AAB59501.1; JOINED.
DR EMBL; M34866; AAB59501.1; JOINED.
DR EMBL; M34867; AAB59501.1; JOINED.
DR EMBL; M34868; AAB59501.1; JOINED.
DR EMBL; M34869; AAB59501.1; JOINED.
DR EMBL; M34870; AAB59501.1; JOINED.
DR EMBL; M34871; AAB59501.1; JOINED.
DR EMBL; M34872; AAB59501.1; JOINED.
DR EMBL; M34873; AAB59501.1; JOINED.
DR HSSP; P05067; IMP.
DR InterPro; IPR001868; A4-APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; Kunitz_BPTI.
DR Pfam; PF00014; Kunitz_BPTI.
DR PRINTS; PR00759; BASICPASE.
DR SMART; SM00006; A4-EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4-EXTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 547 AA; 62135 MW; DB1AIEOFF22D2070 CRC64;

Query Match 69.8%; Score 2831; DB 4; Length 547;
Best Local Similarity 99.18%; Pred. No. 1e-168;
Matches 532; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

OY 1 MLPGIALLLLAAMTAARALEVPTDGNAGLLAEPQJAMFCGRNMNMNONGKWDSPSGTK 60
DB 1 MLPGIALLLLAAMTAARALEVPTDGNAGLLAEPQJAMFCGRNMNMNONGKWDSPSGTK 60
OY 61 TCIDTKEGIILOYCOEYVPELOITNVVEANOPVTIONMCKRGKCKTHPHFVYPRCLVG 120
DB 61 TCIDTKEGIILOYCOEYVPELOITNVVEANOPVTIONMCKRGKCKTHPHFVYPRCLVG 120
OY 121 EFSVADALLVPDKCFLEQERNDVCEYLHMHHTVAKETCSKSTYLAHYGMLPCGIDKFR 180
DB 121 EFSVADALLVPDKCFLEQERNDVCEYLHMHHTVAKETCSKSTYLAHYGMLPCGIDKFR 180
OY 181 GVEFYCCPLAEEESDNDVSADAEEDSDVMWGADTDYADGSEDKVVEAEEVEAEEVEE 240
DB 181 GVEFYCCPLAEEESDNDVSADAEEDSDVMWGADTDYADGSEDKVVEAEEVEAEEVEE 240
OY 241 EADDEDEDEDEVEEAEPEYEATERTSIAITTTTTEVEEYVREVSEQAETGPC 300
DB 241 EADDEDEDEDEVEEAEPEYEATERTSIAITTTTTEVEEYVREVSEQAETGPC 300
OY 301 RAMISRWYEDVTEGKCAPEFYGGCGGNRNNEFTEEYCAVCGSAMQSILKTTEGPLARD 360
DB 301 RAMISRWYEDVTEGKCAPEFYGGCGGNRNNEFTEEYCAVCGSAMQSILKTTEGPLARD 360
OY 361 PVKLPPTTAATSTPDADVDTLETGDENEHAHFOKAKERLEAHRERMSQVMEWEAEERQ 420
DB 361 PVKLPPTTAATSTPDADVDTLETGDENEHAHFOKAKERLEAHRERMSQVMEWEAEERQ 420
OY 421 KNLPRADKAVIOHFOEKVESLEQEAANEQOOLVETHMAVEMALNDRRLALENTYAL 480
DB 421 KNLPRADKAVIOHFOEKVESLEQEAANEQOOLVETHMAVEMALNDRRLALENTYAL 480

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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:55 ; Search time 17.048 Seconds

(without alignments)
1748.833 Million cell updates/sec

Title: US-09-785-215-2

Sequence: 1 MFGGLALLLAAMTARALEV.....KMQNGYENPTYKFFEQMON 770

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	4058	100.0	770 1 A4_HUMAN	P05067 homo sapien
2	3937	97.0	770 1 A4_RAT	P08592 rattus norv
3	3927	96.8	770 1 A4_MOUSE	P12023 mus musculu
4	3921.5	96.6	751 1 A4_SAIUS	Q95241 salimiri sci
5	1981.5	48.8	763 1 APP2_HUMAN	Q06481 homo sapien
6	1971.5	48.6	765 1 APP2_RAT	P15943 rattus norv
7	1704.5	42.0	695 1 APP2_MOUSE	Q06335 mus musculu
8	1155.5	28.5	650 1 APP1_HUMAN	P11693 homo sapien
9	1150.5	28.4	653 1 APP1_MOUSE	Q03157 mus musculu
10	737.5	18.2	886 1 A4_DROME	P14599 drosophila
11	457	11.3	87 1 A4_MACFA	P53601 macaca fasc
12	403	9.9	76 1 A4_MACMU	P29216 macaca mula
13	292	7.2	59 1 A4_BOVIN	Q28053 bos taurus
14	288	7.1	58 1 A4_RABIT	Q28748 oryctolagus
15	288	7.1	58 1 A4_SHEEP	Q28757 ovis aries
16	287	7.1	58 1 A4_CANFA	Q28280 canis famil
17	283	7.0	57 1 A4_PIG	Q29023 sus scrofa
18	283	7.0	57 1 A4_URUMA	Q29149 ursus marit
19	194.5	4.8	3911 1 AKA9_HUMAN	Q29996 h a-kinase
20	186	4.6	252 1 SPT2_HUMAN	Q43291 homo sapien
21	186	4.6	993 1 SCPI_MOUSE	Q62209 mus musculu
22	176	4.3	55 1 ISH1_STOHE	P31713 stoichiactis
23	175.5	4.3	579 1 G160_HUMAN	Q08378 homo sapien
24	175	4.3	302 1 TEPI_RAT	Q02445 rattus norv
25	174.5	4.3	252 1 SPT2_MOUSE	Q35003 mus musculu
26	174.5	4.3	513 1 SPT1_HUMAN	Q43278 homo sapien
27	169	4.2	1875 1 MLPI_YEAST	Q02455 saccharomyc
28	168	4.1	304 1 TEPI_HUMAN	P10646 homo sapien
29	166	4.1	55 1 ISH2_STOHE	P81129 stoichiactis
30	164.5	4.0	507 1 SPT1_MOUSE	Q91097 mus musculu
31	163.5	4.0	346 1 AMBP_MERUN	Q02577 meriones un
32	163.5	4.0	1130 1 YL17_CAEEL	Q11102 caenorhabdi
33	163	4.0	2944 1 CA17_HUMAN	Q02388 homo sapien

34	163	4.0	3176 1 CA36_HUMAN	P12111 homo sapien
35	162	4.0	304 1 TEPI_MACMU	Q28864 macaca mula
36	162	4.0	407 1 IE68_HSVSA	Q01042 herpesvirus
37	162	4.0	3137 1 CA36_CHICK	P15969 gallus gall
38	161.5	4.0	630 1 YCF2_OENVI	P31569 oenothera v
39	161.5	4.0	1278 1 DYNA_HUMAN	Q14203 homo sapien
40	161	4.0	64 1 SPT3_HUMAN	P49223 homo sapien
41	160.5	4.0	721 1 YCF2_OENPI	P31568 oenothera p
42	160	3.9	802 1 NAB3_YEAST	P28986 saccharomyc
43	159	3.9	197 1 MCP1_METCP	P82968 mellithaea c
44	158.5	3.9	2004 1 MOZ_HUMAN	Q92794 homo sapien
45	158	3.9	58 1 ISIK_HELPO	P00994 helix pomat

ALIGNMENTS

RESULT 1
A4_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; Q16011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II)
DE (PN-II) (APP) [Contains: Beta-amyloid protein (beta-APP) (A-beta)].
GN APP OR A4 OR CVAP OR AD1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L.,
RA Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a
RT cell-surface receptor";
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122639; PubMed=2893289;
RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D.,
RA Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F.,
RA Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine
RT proteinase inhibitors";
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,
RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [5]
RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RX MEDLINE=88122640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease";
RL Nature 331:528-530(1988).

[6]
SEQUENCE OF 287-367 FROM N.A.
MEDLINE=88122641; PubMed=2893291;
Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.,
Novel precursor of Alzheimer's disease amyloid protein shows
protease inhibitory activity.",
Nature 331:530-532(1988).
[7]
SEQUENCE OF 284-289 AND 365-770 FROM N.A.
MEDLINE=87231971; PubMed=3035574;
Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.,
Molecular cloning and characterization of a cDNA encoding the
cerebrovascular and the neuritic plaque amyloid peptides.",
Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
[8]
SEQUENCE OF 507-770 FROM N.A.
MEDLINE=88124954; PubMed=2893379;
Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
Marotta C.A.,
Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
disease brain: coding and noncoding regions of the fetal precursor
mRNA are expressed in the cortex.",
Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
[9]
SEQUENCE OF 672-681.
MEDLINE=88035004; PubMed=3312495;
Pairedige W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
Tourtelotte W.W., Huebner V., Shively J.E.,
Amyloid angiopathy of Alzheimer's disease: amino acid composition
and partial sequence of a 4,200-dalton peptide isolated from cortical
microvessels.",
J. Neurochem. 49:1394-1401(1987).
[10]
SEQUENCE OF 739-770 FROM N.A.
MEDLINE=90236318; PubMed=2110105;
Yoshitai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.,
Genomic organization of the human amyloid beta-protein precursor
gene.",
Gene 87:257-263(1990).
[11]
SEQUENCE OF 1-10 FROM N.A.
TISSUE-Layer:
MEDLINE=89016647; PubMed=3140222;
Schon E.A., Mita S., Sadlock J., Herbert J.,
A cDNA specifying the human amyloid beta precursor protein (ABPP)
encodes a 95-kDa polypeptide.",
Nucleic Acids Res. 16:9351-9351(1988).
[12]
SEQUENCE OF 18-50.
MEDLINE=87250462; PubMed=3597385;
van Nostrand W.E., Cunningham D.D.,
Purification of protease nexin II from human fibroblasts.",
J. Biol. Chem. 262:8508-8514(1987).
[13]
IDENTITY OF APP WITH NEXIN-II.
MEDLINE=89384866; PubMed=2506449;
Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
Silba S.,
The secreted form of the Alzheimer's amyloid precursor protein with
the Kunitz domain is protease nexin-II.",
Nature 341:144-147(1989).
[14]
PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
MEDLINE=90211252; PubMed=1969731;
Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.,
Protease-specificity of Kunitz inhibitor domain of Alzheimer's
disease amyloid protein precursor.",
Biochem. Biophys. Res. Commun. 167:716-721(1990).
[15]
COMPLEX WITH G(O).
MEDLINE=93188965; PubMed=8446172;
Nishimoto I., Okamoto T., Matsunura Y., Takahashi S., Okamoto T.,

RA Murayama Y., Ogata E.,
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
RT protein G(O).",
RL Nature 362:75-79(1993).
[16]
X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
MEDLINE=99215582; PubMed=10201399;
Rossjohn J., Cappai R., Fell S.C., Henry A., McKinstry W.J.,
Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
Parker M.W.,
Crystal structure of the N-terminal, growth factor-like domain of
Alzheimer amyloid precursor protein.",
Nat. Struct. Biol. 6:327-331(1999).
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X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
MEDLINE=91104913; PubMed=2125487;
Hynes T.R., Randal M., Kennedy L.A., Eigenbrodt C., Kosiakof A.A.,
X-ray crystal structure of the protease inhibitor domain of
Alzheimer's amyloid beta-protein precursor.",
Biochemistry 29:10018-10022(1990).
[18]
STRUCTURE BY NMR OF 289-344.
MEDLINE=92031488; PubMed=1718421;
Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
Kamarok M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
Tamburini P.P.,
Sequential NMR resonance assignment and structure determination of
the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
precursor protein.",
Biochemistry 30:10467-10478(1991).
[19]
STRUCTURE BY NMR OF 672-699.
MEDLINE=94281210; PubMed=7516706;
Talafoos J., Marciniowski K.J., Klopman G., Zagorski M.G.,
Solution structure of residues 1-28 of the amyloid beta-peptide.",
Biochemistry 33:7788-7796(1994).
[20]
STRUCTURE BY NMR OF 696-706.
MEDLINE=97128622; PubMed=8973180;
Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.,
Three-dimensional structures of the amyloid beta peptide (25-35) in
membrane-mimicking environment.",
Biochemistry 35:16094-16104(1996).
[21]
STRUCTURE BY NMR OF 672-711.
MEDLINE=98359783; PubMed=9693002;
Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.,
Solution structure of amyloid beta-peptide(1-40) in a water-micelle
environment. Is the membrane-spanning domain where we think it is?",
Biochemistry 37:11064-11077(1998).
[22]
STRUCTURE BY NMR OF 672-699.
MEDLINE=20400066; PubMed=10940222;
Poulsen S.-A., Watson A.A., Craik D.J.,
Solution structures in aqueous SDS micelles of two amyloid beta
peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
site.",
J. Struct. Biol. 130:142-152(2000).
[23]
STRUCTURE BY NMR OF 681-706.
MEDLINE=20400065; PubMed=10940221;
Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stinson E.R.,
Lu Y., Felix A.M., Maggio J.E., Lee J.P.,
The Alzheimer's peptide a beta adopts a collapsed coil structure in
water.",
J. Struct. Biol. 130:130-141(2000).
[24]
SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
MEDLINE=88296437; PubMed=2900137;
Dyrks T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.,
Identification, transmembrane orientation and biogenesis of the
amyloid A4 precursor of Alzheimer's disease.",

Query Match 100.0%; Score 4058; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 2, 6e-204;
 Matches 770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 61 T C I D T K E I I L O Y C O E V N P E L O I T N V E A N O P V T I O N M C K R G R K O C K T P H P V I P R C L V G 120
 DB 61 T C I D T K E I I L O Y C O E V N P E L O I T N V E A N O P V T I O N M C K R G R K O C K T P H P V I P R C L V G 120
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 QY 181 G V E F V C C P L A E S D N V S A D A E E D S D V M W G A D T D V A D G S E D K V E A V E E E V A E E E 240
 DB 181 G V E F V C C P L A E S D N V S A D A E E D S D V M W G A D T D V A D G S E D K V E A V E E E V A E E E 240
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 DB 421 K N L R A K D K A V I O H F O E V E S L E O E A N E R O O L V E T H A R Y E A M I N D R R L A L E N Y T A L 480
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 DB 481 Q A V P P R P H V N M L K K Y R A B O K D O H T L K H E H R A M V D P K A A O I R S O V T H L R V I Y E R 540
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 DB 601 K T Y E L L P V N G E F S I D L O P W H S F G A D S V P A N T E N E V P P A R P A A D G L T T R P G S G L T N 660
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 DB 661 I K T E E I S E V K M D A F R H D S G Y E V H H O K L V F A E D V G S K G A I I G L M G V V I A T V I T L 720
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 DB 721 V M L K K O Y T S I H G V E V D A A V T P E R H L S K M O G N Y E N P T Y K F F E O M O N 770

RESULT 2
 A4_RAT STANDARD: PRT: 770 AA.
 AC P08592;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog precursor
 DE (Amyloidogenic glycoprotein) (AG).
 GN APP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=88312583; PubMed=2900758;
 RA Shivers B.D., Hildich C., Muthaup G., Salbaum J.M., Beyreuther K.,
 RA Seeburg P.H.;
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
 RT in rat brain suggests a role in cell contact.";
 RL EMBO J. 7:1365-1370(1988).
 RN [2]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE=89183625; PubMed=2648331;
 RA Kang J., Mueller-Hill B.;
 RT "The sequence of the two extra exons in rat preA4";
 RL Nucleic Acids Res. 17:2130-2130(1989).
 CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; X07648; CA3048.1; -;
 CC EMBL; X14066; CA32229.1; -;
 CC PIR; S00550; S00550.
 CC PIR; S03607; S03607.
 CC HSP; P05067; IAP.
 CC InterPro; IPR001868; A4_APP.
 CC InterPro; IPR002223; Kunitz_BPTI.
 CC Pfam; PF02177; A4_EXTRA; 1.
 CC Pfam; PF00014; Kunitz_BPTI; 1.
 CC PRINTS; PR00203; AMYLOIDA.
 CC PRINTS; PR00755; BASICPTASE.
 CC SMART; SM00006; A4_EXTRA; 1.
 CC SMART; SM00131; KU; 1.
 CC PROSITE; PS00319; A4_EXTRA; 1.
 CC PROSITE; PS00320; A4_INTRA; 1.
 CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE; PS0279; BPTI_KUNITZ_2; 1.
 CC Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 CC Alternative splicing; Serine protease inhibitor.
 CC SIGNAL 1 17
 CC CHAIN 18 770
 CC
 CC FT DOMAIN 18 699
 CC FT TRANSREM 700 723
 CC FT DOMAIN 724 770
 CC FT DOMAIN 673 715
 CC FT DOMAIN 287 345
 CC FT SITE 759 762
 CC FT DISULFID 291 341
 CC FT DISULFID 300 324
 CC FT DISULFID 316 337
 CC FT CARBOHYD 542 571
 CC FT CARBOHYD 571 571
 CC FT VARSPIC 289 289
 CC FT VARSPIC 290 364
 CC SEQUENCE 770 AA; 86704 MW; C26C9D6B2D92947 CRC64;
 Query Match 97.0%; Score 3937; DB 1; Length 770;

Best Local Similarity 96.9%; Pred. No. 5.2e-198;
Matches 746; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

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QY 1 MDPGALLLLAAMTARALEVPTPDNAGLLAPQIAMFGRLMHNHNVONGKWDSPSGTK 60
Db 1 MDPGALLLLAAMTARALEVPTPDNAGLLAPQIAMFGRLMHNHNVONGKWDSPSGTK 60
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Db 61 TCIGKEIILQCOBEVPELOITNVNANOPTIOMNCKRGKCKPTPHVTPRCJLVG 120
QY 121 EFVSALLVPDKCFKFLQERNDVCEPHLHMHTVAKETSEKSTNLHDYGMILPGSIDKFR 180
Db 121 EFVSALLVPDKCFKFLQERNDVCEPHLHMHTVAKETSEKSTNLHDYGMILPGSIDKFR 180
QY 181 GVEFVCCFLAESDNDVSDADAEEDSDVWVGADTDYADGSEDKVVEVAEEVAEVEE 240
Db 181 GVEFVCCFLAESDNDVSDADAEEDSDVWVGADTDYADGSEDKVVEVAEEVAEVEE 240
QY 241 EADDEDEDEDEVEEAEPEEATEERTTSIATTTTTSVEEVEVEVSEQAEETGPC 300
Db 241 EADDEDEDEDEVEEAEPEEATEERTTSIATTTTTSVEEVEVEVSEQAEETGPC 300
QY 301 RAMISRWYFDVTEGKCAFEEYGGCGGNRNNDTEEYCAVGSAMSOSLKTQEPPLARD 360
Db 301 RAMISRWYFDVTEGKCAFEEYGGCGGNRNNDTEEYCAVGSAMSOSLKTQEPPLARD 360
QY 361 PVKLTPTAASPDAVDKLTLEPGDENENAHQAKERLEAKHREMSQVREMEAEQA 420
Db 361 PVKLTPTAASPDAVDKLTLEPGDENENAHQAKERLEAKHREMSQVREMEAEQA 420
QY 421 KNLKRAKKAIVIOHFOEVESLEOEAANEPOLYETHARVEAMNDRRRLALEVITAL 480
Db 421 KNLKRAKKAIVIOHFOEVESLEOEAANEPOLYETHARVEAMNDRRRLALEVITAL 480
QY 481 QAVPRPRHVENMLKKVYRAEQKROHTLKEHVHNVDPKKAQIRSOVMTLHVIER 540
Db 481 QAVPRPRHVENMLKKVYRAEQKROHTLKEHVHNVDPKKAQIRSOVMTLHVIER 540
QY 541 MNOSISILYNPVAVEEIODEVDELQKONYSDVLANMISEPRISGNALMPSLET 600
Db 541 MNOSISILYNPVAVEEIODEVDELQKONYSDVLANMISEPRISGNALMPSLET 600
QY 601 KTYTEILLPVNCEFSLDIOPMHSFGADVSPANTENEVEPVAPRADGLTTPRGSGILT 660
Db 601 KTYTEILLPVNCEFSLDIOPMHSFGADVSPANTENEVEPVAPRADGLTTPRGSGILT 660
QY 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFEADVGSKGAIIIGLVGVVIAIVITL 720
Db 661 IKTEEISEVKMDAEFRHDSGYEVHHOKLVFEADVGSKGAIIIGLVGVVIAIVITL 720
QY 721 VMLKKKQYTSIHGVEVDAAVTPBERLSKMOONGYENPTYKFEQOMON 770
Db 721 VMLKKKQYTSIHGVEVDAAVTPBERLSKMOONGYENPTYKFEQOMON 770

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RESULT 3

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A4_MOUSE
ID A4_MOUSE STANDARD: PRT: 770 AA.
AC P12023;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (Ag).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC STRAIN-BALB/C; TISSUE-Brain;

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RX MEDLINE=92096458; PubMed=1756177;
RA de Strooper B., van Leuven F., van den Berghe H.;
RT "The amyloid beta protein precursor or proteinase nexin II from mouse
RL is closer related to its human homolog than previously reported.";
RN Biochim. Biophys. Acta 1125:141-143(1991).
[12]
RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RC TISSUE-Brain;
RA MEDLINE=88106489; PubMed=3322280;
RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sakaki Y.;
RT "Complementary DNA for the mouse homolog of the human amyloid beta
RL protein precursor.";
RN Biochem. Biophys. Res. Commun. 149:665-671(1987).
[13]
RP REVISIONS.
RA Yamada T.;
RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
[14]
RP SEQUENCE OF 289-364 FROM N.A.
RC STRAIN-CD-1; TISSUE-Placenta;
RX MEDLINE=89345111; PubMed=2569710;
RA Fukuchi K., Martin G.M., Deeb S.S.;
RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
RL precursor of Mus domesticus.";
RN Nucleic Acids Res. 17:5396-5396(1989).
[15]
RP SEQUENCE OF 1-19 FROM N.A.
RX MEDLINE=92209998; PubMed=1555768;
RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
RA Sakai Y.;
RT "Positive and negative regulatory elements for the expression of the
RL Alzheimer's disease amyloid precursor-encoding gene in mouse.";
RN Gene 112:189-195(1992).
[16]
RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE-Brain, and Kidney;
RX MEDLINE=89149813; PubMed=2493250;
RA Yamada T., Sasaki H., Dohura K., Goto I., Sakaki Y.;
RT "Structure and expression of the alternatively-spliced forms of mRNA
RL for the mouse homolog of Alzheimer's disease amyloid beta protein
RT precursor.";
RN Biochem. Biophys. Res. Commun. 158:906-912(1989).
[17]
RP SUBCELLULAR LOCATION: Type I membrane protein.
[18]
RP ALTERNATIVE PRODUCTS: 5 ISOFORMS: APP(395), APP(563), APP(695),
APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
SPLICING.
[19]
RP TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
LIVER.
[20]
RP DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
PHOSPHORYLATION (BY SIMILARITY).
[21]
RP SIMILARITY: BELONGS TO THE APP FAMILY.
[22]
RP SIMILARITY: CONTAINS 1 BP1/KUNITZ INHIBITOR DOMAIN.
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CC
CC EMBL; X59379; -; NOT_ANNOTATED_CDS.
CC
CC EMBL; M18373; AAA37139.1; -
CC
CC EMBL; X15210; CAA33280.1; -
CC
CC EMBL; D10603; BAA01456.1; -
CC
CC EMBL; M24397; AAA39929.1; -
CC
CC PIR; A27485; A27485.
CC
CC PIR; S04855; S04855.
CC
CC PIR; S19727; S19727.

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DR HSSP: P05067; 10CM.
 DR MGD: MGI:88059; App.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 DR Glycoprotein: Amyloid; Neurone; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17
 FT CHAIN 18 770
 FT DOMAIN 18 699
 FT TRANSMEM 700 723
 FT DOMAIN 724 770
 FT DOMAIN 673 715
 FT DOMAIN 287 345
 FT SITE 759 762
 FT DISULFID 291 341
 FT DISULFID 300 324
 FT DISULFID 316 337
 FT CARBOHYD 542 542
 FT CARBOHYD 571 571
 FT VARSPLIC 289 289
 FT VARSPLIC 290 364
 FT VARSPLIC 346 380
 SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAFA CRC64;

Query Match 96.8%; Score 3927; DB 1; Length 770;
 Best Local Similarity 96.8%; Pred. No. 1.7e-197;
 Matches 745; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 MDEGLALLLAAMTARALEVPTDGNAGLAEPOIAMECGRLNMNMNONGKWDSPSGTK 60
 DB 1 MDEGLALLLAAMTARALEVPTDGNAGLAEPOIAMECGRLNMNMNONGKWDSPSGTK 60
 QY 61 TCIDTKEGIIYOCEVYPELOITNVANOPVTIONMCKRGKCKHPPHVIYRCLVG 120
 DB 61 TCIDTKEGIIYOCEVYPELOITNVANOPVTIONMCKRGKCKHPPHVIYRCLVG 120
 QY 121 EFVSDALLVDPCKKFLHQRMDVCETHLHMTYAKETCSEKSTNLHDYGMLLPCGIDKFR 180
 DB 121 EFVSDALLVDPCKKFLHQRMDVCETHLHMTYAKETCSEKSTNLHDYGMLLPCGIDKFR 180
 QY 181 GVEVYCCPLAEESNVDSADAEEDSDVWVGADTYADGSEDKYVEAEVEEVAEVEE 240
 DB 181 GVEVYCCPLAEESNVDSADAEEDSDVWVGADTYADGSEDKYVEAEVEEVAEVEE 240
 QY 241 EADDEDEDEGDEVEEAEPEYEATERTSIATTTTTESVEEVRREVCSOAEATGPC 300
 DB 241 EADDEDEDEGDEVEEAEPEYEATERTSIATTTTTESVEEVRREVCSOAEATGPC 300
 QY 301 RAMISRYFDYTEKCAPFFYGGCGGNRNNDEEYCAVGSAMSOSLKTTOEPLARD 360
 DB 301 RAMISRYFDYTEKCAPFFYGGCGGNRNNDEEYCAVGSAMSOSLKTTOEPLARD 360
 QY 361 PVKLPPTAASTPPADVKKYLETPGDENHAFHOKAKERLEAKHRRMSQVAREAEAROA 420
 DB 361 PVKLPPTAASTPPADVKKYLETPGDENHAFHOKAKERLEAKHRRMSQVAREAEAROA 420
 QY 421 KNPDKAKKAVIOHFQOKVSVLEOEANERQOLVETHMAREALNRRRLALENTYITAL 480
 DB 421 KNPDKAKKAVIOHFQOKVSVLEOEANERQOLVETHMAREALNRRRLALENTYITAL 480
 QY 481 QAVPPRRHVENMLKKYVRAEQKDRQHTLKFHEHVRVNDPKKAAQIRSOVTHLRYIER 540
 DB 481 QAVPPRRHVENMLKKYVRAEQKDRQHTLKFHEHVRVNDPKKAAQIRSOVTHLRYIER 540

DB 481 QAVPPRRHVENMLKKYVRAEQKDRQHTLKFHEHVRVNDPKKAAQIRSOVTHLRYIER 540
 QY 541 MNOSLSILYVPAVAEIOEVEDELLQEKONYSDVLIANNISPRISYGDALMPSLTER 600
 DB 541 MNOSLSILYVPAVAEIOEVEDELLQEKONYSDVLIANNISPRISYGDALMPSLTER 600
 QY 601 KTTVELLPVNGEESLDDILOPMHSFGADSVAPNANENEVEPADAPADRGLTTPRGSLTN 660
 DB 601 KTTVELLPVNGEESLDDILOPMHSFGADSVAPNANENEVEPADAPADRGLTTPRGSLTN 660
 QY 661 IKTEEISEVMKDAEFHRDSCGEVYHOKLYFAEDVGSNKGAIIGLMGVAVIATVITL 720
 DB 661 IKTEEISEVMKDAEFHRDSCGEVYHOKLYFAEDVGSNKGAIIGLMGVAVIATVITL 720
 QY 721 VMLKKQYTSIHGGVYEVDAAVTPPEERHLSKMOONGYENTTYFFEQMON 770
 DB 721 VMLKKQYTSIHGGVYEVDAAVTPPEERHLSKMOONGYENTTYFFEQMON 770
 DB 721 VMLKKQYTSIHGGVYEVDAAVTPPEERHLSKMOONGYENTTYFFEQMON 770

RESULT 4
 A4_SAISC
 ID A4_SAISC STANDARD; PRT; 751 AA.
 AC O95241;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein precursor [contains: Beta-amyloid protein (beta-Ap) (A-beta)].
 GN App.
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver, and Kidney;
 RX MEDLINE=96108492; PubMed=8532114;
 RA Levy E., Amorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy";
 RL Neurobiol. Aging 16:805-808(1995).
 CC -1- FUNCTION: FUNCTIONAL, NEURONAL, RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC -----
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 CC -----
 DR EMBL: S81024; AAD14347.1; -.
 DR HSSP: P05067; 1AAP.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.

DR PROSITE; PS0280; BPT1_KUNITZ_1; 1.
 DR PROSITE; PS50279; BPT1_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
 KW Signal; Serine protease inhibitor.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 751 A4 PROTEIN.
 FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 681 704 POTENTIAL.
 FT DOMAIN 705 751 CYTOSOLASMIC (POTENTIAL).
 FT SITE 287 345 BPT1/KUNITZ INHIBITOR.
 FT ACT_SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
 FT DISULFID 291 341 REACTIVE BOND.
 FT DISULFID 300 324 BY SIMILARITY.
 FT DISULFID 316 337 BY SIMILARITY.
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
 FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
 SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;
 Query Match 96.6%; Score 3921.5; DB 1; Length 751;
 Best Local Similarity 96.9%; Pred. No. 3.2e-197;
 Matches 746; Conservative 2; Mismatches 3; Indels 19; Gaps 1;
 Oy 1 MLPGIALLLAAMTARALEVPTDGNAGLLABPOIAMFCGRIMHNNVONGKWDSPSGTK 60
 1 MLPGIALLLAAMTARALEVPTDGNAGLLABPOIAMFCGRIMHNNVONGKWDSPSGTK 60
 Db 1 MLPGIALLLAAMTARALEVPTDGNAGLLABPOIAMFCGRIMHNNVONGKWDSPSGTK 60
 Oy 61 TCIDTKEEIIIOCOEYVELOITNVENANOVPTIONMCKRGKCKTHPHVIRCLVG 120
 61 TCIDTKEEIIIOCOEYVELOITNVENANOVPTIONMCKRGKCKTHPHVIRCLVG 120
 Db 61 TCIDTKEEIIIOCOEYVELOITNVENANOVPTIONMCKRGKCKTHPHVIRCLVG 120
 Oy 121 EFVSADALVPKCKFLHGRMDVCEYHMHYVAKETSEKSTNHDGMLPGIDKFR 180
 121 EFVSADALVPKCKFLHGRMDVCEYHMHYVAKETSEKSTNHDGMLPGIDKFR 180
 Db 121 EFVSADALVPKCKFLHGRMDVCEYHMHYVAKETSEKSTNHDGMLPGIDKFR 180
 Oy 181 GVEFVCCPLAEESDNDVSDAEEDSDVMWGADTDYADGSEDKVEVEEVEVEE 240
 181 GVEFVCCPLAEESDNDVSDAEEDSDVMWGADTDYADGSEDKVEVEEVEVEE 240
 Db 181 GVEFVCCPLAEESDNDVSDAEEDSDVMWGADTDYADGSEDKVEVEEVEVEE 240
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 181 GVEFVCCPLAEESDNDVSDAEEDSDVMWGADTDYADGSEDKVEVEEVEVEE 240
 Db 181 GVEFVCCPLAEESDNDVSDAEEDSDVMWGADTDYADGSEDKVEVEEVEVEE 240
 Oy 241 EADDEDEDEDEVEEKEEPEYETETTSIATTTTTTSVEEVNAEVCSEQAETGPC 300
 241 EADDEDEDEDEVEEKEEPEYETETTSIATTTTTTSVEEVNAEVCSEQAETGPC 300
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 241 EADDEDEDEDEVEEKEEPEYETETTSIATTTTTTSVEEVNAEVCSEQAETGPC 300
 Db 241 EADDEDEDEDEVEEKEEPEYETETTSIATTTTTTSVEEVNAEVCSEQAETGPC 300
 Oy 301 RAMISRWFEVDTGEGCAFEYGGCGGNRNNDTEFEYCAVNGSAMSGLLTTQDEPLARD 360
 301 RAMISRWFEVDTGEGCAFEYGGCGGNRNNDTEFEYCAVNGSAMSGLLTTQDEPLARD 360
 Db 301 RAMISRWFEVDTGEGCAFEYGGCGGNRNNDTEFEYCAVNGSAMSGLLTTQDEPLARD 360
 Oy 301 RAMISRWFEVDTGEGCAFEYGGCGGNRNNDTEFEYCAVNGSAMSGLLTTQDEPLARD 360
 301 RAMISRWFEVDTGEGCAFEYGGCGGNRNNDTEFEYCAVNGSAMSGLLTTQDEPLARD 360
 Db 301 RAMISRWFEVDTGEGCAFEYGGCGGNRNNDTEFEYCAVNGSAMSGLLTTQDEPLARD 360
 Oy 361 PVKLPPTAASPDAVDKYLETPGDENEHAFHOKAKERLEAKHREMSQVMEWEAEERQA 420
 361 PVKLPPTAASPDAVDKYLETPGDENEHAFHOKAKERLEAKHREMSQVMEWEAEERQA 420
 Db 361 PVKLPPTAASPDAVDKYLETPGDENEHAFHOKAKERLEAKHREMSQVMEWEAEERQA 420
 Oy 361 PVKLPPTAASPDAVDKYLETPGDENEHAFHOKAKERLEAKHREMSQVMEWEAEERQA 420
 361 PVKLPPTAASPDAVDKYLETPGDENEHAFHOKAKERLEAKHREMSQVMEWEAEERQA 420
 Db 361 PVKLPPTAASPDAVDKYLETPGDENEHAFHOKAKERLEAKHREMSQVMEWEAEERQA 420
 Oy 421 KNLFRADKKAIVIOHFOEVESELEBOANERQOLVETIHARVEMALNDRRLALENYITAL 480
 421 KNLFRADKKAIVIOHFOEVESELEBOANERQOLVETIHARVEMALNDRRLALENYITAL 480
 Db 421 KNLFRADKKAIVIOHFOEVESELEBOANERQOLVETIHARVEMALNDRRLALENYITAL 480
 Oy 421 KNLFRADKKAIVIOHFOEVESELEBOANERQOLVETIHARVEMALNDRRLALENYITAL 480
 421 KNLFRADKKAIVIOHFOEVESELEBOANERQOLVETIHARVEMALNDRRLALENYITAL 480
 Db 421 KNLFRADKKAIVIOHFOEVESELEBOANERQOLVETIHARVEMALNDRRLALENYITAL 480
 Oy 481 QAVPRPRHVNMMKKYRAEOKROHTLKHENRYMDPKKAQIRSQVMTLRYIER 540
 481 QAVPRPRHVNMMKKYRAEOKROHTLKHENRYMDPKKAQIRSQVMTLRYIER 540
 Db 481 QAVPRPRHVNMMKKYRAEOKROHTLKHENRYMDPKKAQIRSQVMTLRYIER 540
 Oy 481 QAVPRPRHVNMMKKYRAEOKROHTLKHENRYMDPKKAQIRSQVMTLRYIER 540
 481 QAVPRPRHVNMMKKYRAEOKROHTLKHENRYMDPKKAQIRSQVMTLRYIER 540
 Db 481 QAVPRPRHVNMMKKYRAEOKROHTLKHENRYMDPKKAQIRSQVMTLRYIER 540
 Oy 541 MNGSLSTLYNPAVAEELIODEVDELLOEKONYSDVLANMISEPRISYNDALMPSLLET 600
 541 MNGSLSTLYNPAVAEELIODEVDELLOEKONYSDVLANMISEPRISYNDALMPSLLET 600
 Db 541 MNGSLSTLYNPAVAEELIODEVDELLOEKONYSDVLANMISEPRISYNDALMPSLLET 600
 Oy 541 MNGSLSTLYNPAVAEELIODEVDELLOEKONYSDVLANMISEPRISYNDALMPSLLET 600
 541 MNGSLSTLYNPAVAEELIODEVDELLOEKONYSDVLANMISEPRISYNDALMPSLLET 600
 Db 541 MNGSLSTLYNPAVAEELIODEVDELLOEKONYSDVLANMISEPRISYNDALMPSLLET 600
 Oy 601 KTYVELLPVNEEFLDLDQPHSGADSVPAANTEVEVPVAPARADGLTTRPGSGLTN 660
 601 KTYVELLPVNEEFLDLDQPHSGADSVPAANTEVEVPVAPARADGLTTRPGSGLTN 660
 Db 601 KTYVELLPVNEEFLDLDQPHSGADSVPAANTEVEVPVAPARADGLTTRPGSGLTN 660
 Oy 601 KTYVELLPVNEEFLDLDQPHSGADSVPAANTEVEVPVAPARADGLTTRPGSGLTN 660
 601 KTYVELLPVNEEFLDLDQPHSGADSVPAANTEVEVPVAPARADGLTTRPGSGLTN 660
 Db 601 KTYVELLPVNEEFLDLDQPHSGADSVPAANTEVEVPVAPARADGLTTRPGSGLTN 660
 Oy 661 IKTEEISEVKMDAEFRHDSGEVYHOKLVFAEDVGNKGAIIIGLVGVVIAIVITL 720
 661 IKTEEISEVKMDAEFRHDSGEVYHOKLVFAEDVGNKGAIIIGLVGVVIAIVITL 720
 Db 661 IKTEEISEVKMDAEFRHDSGEVYHOKLVFAEDVGNKGAIIIGLVGVVIAIVITL 720
 Oy 661 IKTEEISEVKMDAEFRHDSGEVYHOKLVFAEDVGNKGAIIIGLVGVVIAIVITL 720
 661 IKTEEISEVKMDAEFRHDSGEVYHOKLVFAEDVGNKGAIIIGLVGVVIAIVITL 720
 Db 661 IKTEEISEVKMDAEFRHDSGEVYHOKLVFAEDVGNKGAIIIGLVGVVIAIVITL 720
 Oy 721 VMLKKOYTSIHGVEVDAVTPPEERHLSKMOONGYENPTYKFEEDOMN 770
 721 VMLKKOYTSIHGVEVDAVTPPEERHLSKMOONGYENPTYKFEEDOMN 770
 Db 721 VMLKKOYTSIHGVEVDAVTPPEERHLSKMOONGYENPTYKFEEDOMN 770

Db 702 VMLKKOYTSIHGVEVDAVTPPEERHLSKMOONGYENPTYKFEEDOMN 751
 |||||
 RESULT 5
 APP2_HUMAN STANDARD; PRT; 763 AA.
 AC APP2_HUMAN
 ID 006481;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH)
 DE (CDEI-box binding protein) (CDEBP).
 GN APP2 OR APP2L
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=93250009; Pubmed=8485127;
 RA Sprecher C.A., Grant F.J., Grimm G., O'Hara P.J., Norris F.,
 RA Norris K., Foster D.C.;
 RT "Molecular cloning of the cDNA for a human amyloid precursor protein
 RT homolog: evidence for a multigene family.";
 RL Biochemistry 32:4481-4486(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=95217334; Pubmed=7702756;
 RA von der Kammer H., Hanes J., Klaudiny J., Schelt K.H.;
 RT "A human amyloid precursor-like protein is highly homologous to a
 RT mouse specific DNA-binding protein.";
 RL DNA Cell Biol. 13:1137-1143(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94035131; Pubmed=8220435;
 RA Masco W., Gurubagavata S., Paradis M., Romano D.M., Sisodia S.S.,
 RA Hyman B.T., Neve R.L., Tanzi R.E.;
 RT "Isolation and characterization of APLP2 encoding a homologue of the
 RT Alzheimer's associated amyloid beta protein precursor.";
 RL Nat. Genet. 5:95-99(1993).
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF HEMOSTASIS. THE
 CC SOLUBLE FORM MAY HAVE INHIBITORY PROPERTIES TOWARDS COAGULATION
 CC FACTORS. MAY INTERACT WITH CELLULAR G-PROTEIN SIGNALING PATHWAYS.
 CC MAY BIND TO THE DNA 5'-GTGACATG-3'(CDEI BOX).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
 CC (POTENTIAL).
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS, 1 (SHOWN HERE), 2 AND
 CC 3, ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: IN PLACENTA, BRAIN, HEART, LUNG, LIVER, KIDNEY
 CC AND ENDOTHELIAL TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPT1/KUNITZ INHIBITOR DOMAIN.
 CC -----
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 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; S60099; AAC60589.1; -;
 CC EMBL; L09209; AAA3526.1; -;
 CC EMBL; 222572; CAA80295.1; -;
 CC EMBL; L27631; AAC41701.1; -;
 CC HSSP; P05067; 1MWP.
 CC MIM; 104776; -;
 CC InterPro; IPR001868; A4_APP.
 CC InterPro; IPR002223; Kunitz_BPT1.

DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Transmembrane; Signal; Alternative splicing; DNA-binding;
 KW Nucleic acid; Serine protease inhibitor.
 FT SIGNAL 1 29
 FT CHAIN 30 763
 FT DOMAIN 30 692
 FT TRANSMEM 693 716
 FT DOMAIN 717 763
 FT DOMAIN 215 280
 FT DOMAIN 215 231
 FT ACT_SITE 320 321
 FT DISULFID 310 360
 FT DISULFID 319 343
 FT DISULFID 335 356
 FT VARSPIC 308 363
 FT VARSPIC 613 624
 FT CONFLICT 543 543
 SQ SEQUENCE 763 AA; 86955 MW; CA3A/D6DB8A28B0 CRCS4;

Query Match 48.8%; Score 1981.5; DB 1; Length 763;
 Best Local Similarity 50.4%; Pred. No. 3,2e-96;
 Matches 408; Conservative 127; Mismatches 168; Indels 107; Gaps 21;

QY 5 LALLLAAAPAALEV-----PTDGNAG--LAEPOIAEFGSLNHNMYNQSKWSDP 56
 DB 15 LALLLGLALAPALALAGLYEALANAGTGFAVAEPOIAEFGSLNHNMYNQSKWSDP 74
 QY 57 SGFTCTIDTEGILYOEOEVRELOITNYVANORPTIONKSKRGYKSKNHFVLYR 116
 DB 75 TGTSCSETEEEVLOYOEMRELOITNYVANORPTIONKSKRGYKSKNHFVLYR 132
 QY 117 CLVGEFVSADLLVPDKCKFLHQRMDVCETHLHWTVAKETCSKSTNLNDYGMILPCGI 176
 DB 133 CLVGEFVSADLLVPDKCKFLHQRMDVCETHLHWTVAKETCSKSTNLNDYGMILPCGI 192
 QY 177 DKRGVEFVCCPLAESDNDSDADBDSDVMWGADTDYADGSEDKVVEVAEEVEAE 236
 b 193 DOFHGTGVCCPQTKIIGSVSKSEEEDEE-----EEEEDEDEDDYDYKSEFTEAD 245
 237 VEE--EEA--DDDDDDDDGDEVEEAE-----EPEEATERTTSTATTTTTTSVE 284
 DB 246 LEDTEEAVDDEDEDEEVEEDRDYDTPFKGDDNE--ENPTERGSGTMSDEIT 303
 QY 285 EVVEVEVSEQAETGPRAMISRMVFDVTEGKCAPFFYGGCGGNNNDTEVEYCAVCGSA 344
 DB 304 HDVAAGVSGEAMGRCRAVMRWFDLSKGCVRFTYGGCGGNNNDTEVEYCAVCGSA 363
 QY 345 MSOSLKTTOEPLARDVYKLTAASTPDADVKLTLEPGDENHAFHOKAKERLEAKHRE 404
 DB 364 I-----PPTPLPT-----NDVYFETTSADNNEHARFQKAEQLEIRHRN 403
 QY 405 RMSQVMEWEAEARQAKNLPRADKKAVIQHQQEVESELEQANERQOLVTHNARVEM 464
 DB 404 RMSQVMEWEAEARQAKNLPRADKKAVIQHQQEVESELEQANERQOLVTHNARVEM 463
 QY 465 LNDRRRLALENYITALQAVPRPRHVEMLKRYRAEOKDRQHLKFNHNVAVDPKKA 524
 DB 464 LNDRRRLALENYITALQAVPRPRHVEMLKRYRAEOKDRQHLKFNHNVAVDPKKA 523
 QY 525 QIRSQVTHLAVYIERKNSISLLYNPAVAEETQDEYDELQEQNTSDVLANMISER 584
 DB 524 QIRSQVTHLAVYIERKNSISLLYNPAVAEETQDEYDELQEQNTSDVLANMISER 572

QY 585 RISYNDALMPSLETETVTELLPVNGEFSLLDLPMSHSGADSVAPANTENEVEVPDAR 644
 DB 573 -----DQFASISERTVDR---VSSEES-EEIPRHPF--HFPALPENE-----DTPQ 616
 QY 645 AADRGLTRPGSGITN-----IKTEE--ISEYKDAEPRHDSGYEVHOKLVEFADVG 696
 DB 617 ELYHPM--KKSGVGEGDGLIGAEKVKNSKNKVDENMVDETLVD--KEMINARVGG 672
 QY 697 S-----NKGATIGLVAGGVATVIVITLMLKKQOYSHHGVYEVD 739
 DB 673 GLEERESVGPLREDFSLSSALGLIVAVATVIVISLMLKKQOYSHHGVYEVD 732
 QY 740 AAVTPEERHLSKMOQNGENPTYKFEQOMQ 769
 DB 733 PMLTPEERHLSKMOQNGENPTYKFEQOMQ 762

RESULT 6
 APP2_RAT ID STANDARD; PRT; 765 AA.
 AC p15943;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Amyloid-like protein 2 precursor (Sperm membrane protein YMK-II).
 GN APLP2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE OF 1-627 FROM N.A.
 RC STRAIN=WISTAR; TISSUE=Brain, and Heart;
 RX MEDLINE=9436849; PubMed=8086458;
 RA Sandbriink R., Masters C.L., Beyreuther K.;
 RT "Complete nucleotide and deduced amino acid sequence of rat amyloid protein precursor-like protein 2 (APLP2/APPH): two amino acids length difference to human and murine homologues."; Biochim. Biophys. Acta 1219:167-170(1994).
 RL [2]
 RN SEQUENCE OF 575-765 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=90207205; PubMed=1690887;
 RA Van Y.C., Bai Y., Wang L.F., Miao S.Y., Koide S.S.;
 RT "Characterization of cDNA encoding a human sperm membrane protein related to A4 amyloid protein."; Proc. Natl. Acad. Sci. U.S.A. 87:2405-2408(1990).
 RL CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS: A (SHOWN HERE), B, C AND D;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC
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 CC
 DR EMBL; X77934; CA54906.1; -;
 DR EMBL; M31322; AAA42352.1; -;
 DR PIR; A35981; A35981.
 DR HSSP; P05067; 1MMP.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.

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DR PROSITE: PS00319; A4-EXTRA; 1.
DR PROSITE: PS00320; A4-INTA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Transmembrane: Alternative splicing; Serine protease inhibitor;
KW Signal: Glycoprotein.
FT SIGNAL 1 29
FT CHAIN 1 765
FT DOMAIN 30 695
FT TRANSMEM 696 718
FT DOMAIN 719 765
FT DOMAIN 218 282
FT DOMAIN 308 366
FT ACT_SITE 322 323
FT DISULFID 312 362
FT DISULFID 321 345
FT DISULFID 337 358
FT DOMAIN 218 229
FT CARBOHYD 628 628
FT VARSPIC 311 365
FT VARSPIC 616 627
FT CONFLICT 575 577
SQ SEQUENCE 765 AA; 86882 MW; CFS1PCCCE305A0CF CRC64;

Query Match 48.6%; Score 1971.5; DB 1; Length 765;
Best Local Similarity 49.7%; Pred. No. 1,1e-95;
Matches 401; Conservative 134; Mismatches 173; Indels 99; Gaps 20;

QY 5 LALLLLAMTARALEV-----PTQGNAG--LLAEPOIAMCGRLMMNNQNGKWDSDP 56
DB 15 LVLVLLGLTLPALALAGYIEALANAGTGRAVAEPQIAMCGRLMMNNVQTGTGWEEDP 74
QY 57 SGTCTCIDTKESIGLOCEVYPELOITNVVNEAPVTIONCKRGKCKTHPHFVPIYR 116
DB 75 TGTSCICLTKEVLOLQCEIYPELOITNVMEANQPVNIDSMCRKQKCRS--HIVIEFK 132
QY 117 CLVGFVSDALLVPKCKFLHOERNDVCETHLHMTVAKETCSKSTNLHMDGLMPCGI 176
DB 133 CLVGFVSDVLLVPENCQFHOERMEVCEKHQRHMTVYKALCTGMLTYSYGMLLPCGV 192
QY 177 DKFRGVFVCCPLAE--TSDNVSADAEEDSDVWNGADDTYA--DGSDDKVAEAESEE 233
DB 193 DOFHETEVYCCQTKRVNDSSTMSKEEEEEE---DEEDYADLCKSEFPPEADLEDT 248
QY 234 VAEVEEERADDEDEDEDEVEEAEPEYEE-----ATERTSTATTYTTTTSVEEVY 287
DB 249 EAAADEDEDEEEEBEBEVEEDRDYYDSFKGDYNEENTERSDGTISDKRIANDV 308
QY 288 REVCEQAEETGPCRAMISRWFVDTGKCAPEFYGGCGGNRNFTDEYCAVCGSAMSQ 347
DB 309 KAVCSQEAETGPCRAMSRWFVDTGKCAPEFYGGCGGNRNFTDEYCAVCGSAMSQ 366
QY 348 SLKTKTQEPRLARDPKLTPTASTPDVAIDKYLEPQGDENEHHPKAEERLAKRREMS 407
DB 367 -----PPTPLPT-----NDVDVIFETISADONEHARFKAQEQLTIRHRSMD 408
QY 408 QVMEWEAEARQAKNLPKADKAVIOTHOEKEVSELEQEAERQOOLVTHMARVAMIND 467
DB 409 RKKKMEWEAELOAKNLPRAERQTLQHOQAVKALEKEASEKQOLVETHLARVAMIND 468
QY 468 RRRRLALENTITALQAVPPRRHVENMLKKYVAEOKDRQHTLKHFEHVMVDPKKAQIR 527
DB 469 RRRRLALENTITALQAVPPRRHVENMLKKYVAEOKDRQHTLKHFEHVMVDPKKAQIR 528
QY 528 SOVTHLVITVIERMNOSSILLYNPAVAEETODEVELLOKQONSDVLANMISERIS 587
DB 529 SOVTHLVITVIERMNOSSILLYNPAVAEETODEVELLOKQONSDVLANMISERIS 587
QY 588 YGNDAIMPSTETTKTVLLPENGSESLDDLOPMHSGADSVAPANTENEVEVDARPAAD 647
DB 589 YGNDAIMPSTETTKTVLLPENGSESLDDLOPMHSGADSVAPANTENEVEVDARPAAD 647
QY 595 ---DQFTSSISBNPDV---VSSSES--EELPDPHFP--HPPPSLSSEB---DQDPFLY 621
DB 595 ---DQFTSSISBNPDV---VSSSES--EELPDPHFP--HPPPSLSSEB---DQDPFLY 621
QY 648 RGLTTPGSGLTN-----IKTEE---ISEVKDAEFRRDSDGYEVHMQKLVEFAEDVGS-- 697
DB 648 RGLTTPGSGLTN-----IKTEE---ISEVKDAEFRRDSDGYEVHMQKLVEFAEDVGS-- 697

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DB 622 HPM--KKGSGNAEDDGLCAEKEVYNSKNKMDENMVIDETLDV--KEMIFNAERVGLE 677
QY 698 -----NKAIIIGMVGVIATVITVITVLMKKKQYTSIHNGVYEVDAV 742
DB 678 EEPDSVGLREDPFLSSSLGALVAIVATVIVISLMLKRYGTISHGIVEVHML 737
QY 743 TPEERHLSKMOONGYENPTVYKFFEQMQ 769
DB 738 TPEERHLSKMOONGYENPTVYKFFEQMQ 764

RESULT 7
APP2_MOUSE STANDARD; PRT; 695 AA.
AC 006335;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Amyloid-like protein 2 precursor (CDEI-box binding protein) (CDEBP).
GN APP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Fetal brain;
RL von der Kammer H.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-246 FROM N.A.
RX MEDLINE=94032480; PubMed=8218408;
RA Hanes J., von der Kammer H., Kristjansson G.I., Scheit K.H.;
RT "The complete cDNA coding sequence for the mouse CDEI binding
RT protein."
RL Biochim. Biophys. Acta 1216:154-156(1993).
RN [3]
RP SEQUENCE OF 185-695 FROM N.A.
RX STRAIN=BALB/C; Tissue=Heart;
RA MEDLINE=93129193; PubMed=1482349;
RA Vidal F., Blangy A., Rassoulzadegan M., Guzin F.;
RT "A murine sequence-specific DNA binding protein shows extensive local
RT similarities to the amyloid precursor protein."
RL Biochem. Biophys. Res. Commun. 189:1336-1341(1992).
RN [4]
RP SEQUENCE OF 1-35 FROM N.A.
RX STRAIN=129/SV;
RX MEDLINE=96029629; PubMed=7592716;
RA von Koch C.S., Jahiri D.K., Mammen A.L., Copeland N.G.,
RA Gilbert D.J., Jenkins N.A., Sisodia S.S.;
RT "The mouse APP2 gene. Chromosomal localization and promoter
RT characterization."
RL J. Biol. Chem. 270:25475-25480(1995).
CC -1- FUNCTION: BINDS TO THE DNA 5'-GTCAATG-3' (CDEI BOX) WHICH PLAYS
CC AN IMPORTANT ROLE IN THE EARLY DEVELOPMENT OF EMBRYOS.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND NUCLEAR
CC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: 222592; CAAB0306.1; -
DB EMBL: M97216; AAA20039.1; -
DB EMBL: U34291; AAC52318.1; -
DB PIR: JC1404; JC1404.
DB HSSP: P05067; 1MP.

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DR MGD; MGI:88047; A0JD2.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
KM Transmembrane; DNA-binding; Signal; Nuclear protein.
DR SIGNAL 1 29
FT CHAIN 30 695
FT DOMAIN 30 624
FT TRANSMEM 625 648
FT DOMAIN 649 695
FT DOMAIN 218 294
FT DOMAIN 218 231
FT DOMAIN 256 266
FT CARBOHYD 485 485
FT CONFLICT 185 189
FT SEQUENCE 695 AA; 78944 MW; B8F4B95AAB2A0311 CRC64;

Query Match 42.08; Score 1704.5; DB 1; Length 695;
Best Local Similarity 46.98; Pred. No. 7,5e-82;
Matches 371; Conservative 113; Mismatches 170; Indels 137; Gaps 24;

QY 5 LALLLLAAMTAAALEV-----PTDGNAG---LAEPIAMFCGRLLNMHVNQNGKMSDP 56
DB 15 LVLVLLGLTPAALALGYDEALANAGTGAFAVEPIALMCGKLNHVNITGKWEPP 74
QY 57 SGTFTCIDTEGLIYOCEVYPELQITNVVEANOPVITOMKSGRQCKTHPHEVYR 116
DB 75 TGTSCSGCTKEEVLYOCEIPELQITNVVEANOPVINDSCRRDKCKSCKS -HIVLPK 132
QY 117 CLVGEFSDALIVNDCRKLHQRNDYCEHLMHTYAKESCKSKNLNDYGLMCCGI 176
DB 133 CLVGEFSDVLLVNDNQCFHQEEMVECEKQRNHTLVKCEGLTLYSYGLMCCGV 192
QY 177 DKFGEVFCVCPPLAESDNDVSADAEEDSDVMWGADTDVADGSECKVVEAEVEVAE 236
DB 193 DQFNGTEVCCP---QTKYDS-----DSTMSK-----DEEE--- 221
QY 237 VEEEDADDEDEDEGEVEEAEPEEATERTTSTATTTTTTSEVEEVREVCBOAE 296
DB 222 -EEDEDEDEEDYDLDSPEPTADLEDTFE--AAADEEEDDEGEVEVED----- 270
QY 297 TGCPRAMISRYEYVTEBCKAPFYGGCGGRNNFDEEYCMANVCGSMGSLKTTQEP 356
DB 271 -----RDYYXD-----PF---KGDYNEENFTE-----PSSGCTI--SDKE 301
QY 357 LARDPVKLTPTAASTPDAVDKYLETPGDENHAFHOKAKERLEAKHREBMSQVREWEBA 416
DB 302 IVHD-VAVPPTPLPTND-VDYLETTSADNDENHAFHOKAKERLEAKHREBMSQVREWEBA 359
QY 417 EROAKNLPRKADKKAIVIOHFOEKVESLEQEAANERQOLVETHMAVEAMLDNRRLALENY 476
DB 360 ELQAKNLPRKTERQTLIOHFOAMVAKLEKASEKQOLVETHLAVEMALNDRRLALENY 419
QY 477 ITAQAVPRPRHAFVNLKAVRAEOKDRQTLTKHEFVRAVNDKKAQISQVMTHLRV 536
DB 420 LAAQSDPRPRHRLQALRVRAENKDRHTLTHYQHLVAVDEKKAQMSQVMTHLRV 479
QY 537 IYERNQSLSLVNVPAVEEIODEVDELQKEQNSDDVLANMISPRISYGDALMPS 596
DB 480 IEEFRNOSTLTLKVPVVAQETIOEIEIDELQOR--ADM-----DQFTSS 522
QY 597 LLETKTVELLPVNGEFLDLDLPWHSFGADSPANTENEVEPYDARPADRLTTPGGS 656
DB 523 ISENPVAVRVSSESE--EIPFPHLHPF-----PSLSENE-----GSGMAEDG- 565
QY 657 GLTIKITEEI-SEYKMAEFHDSGYEYHNOKLVPAEDVS-----N 698
DB 566 GLIAEERKVNISKKNKMDENNVITDELVD--KEMIFNAERVGGLDEEBSGRLREDPSLS 623
QY 699 KGAIIGLVGQVVIATVIVITLVMLKKQYTSIHNGVEVDAVTPREHRLSKMQONGYE 758

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DB 624 SNMLIGLVAVAIATVIVITLVMLKKRQYGTISHGLVEVDPLTPREHRLNKNQNGYE 683
QY 759 NPTYKFEEDQ 769
DB 684 NPTYKYLEQMO 694

RESULT 8
APPL_HUMAN
ID APPL_HUMAN STANDARD; PRT; 650 AA.
AC P51693; 000113;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Amyloid-like protein 1 precursor (APLP).
GN APLP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98088960; PubMed=9428684;
RA Paliga K., Peraus G., Krieger S., Duwrtwang U., Hesse L., Multhaup G.,
RA Masters C.L., Beyreuther K., Weidemann A.;
RT "Human amyloid precursor-like protein 1--cDNA cloning, ectopic
RT expression in COS-7 cells and identification of soluble forms in the
RT cerebrospinal fluid.";
RL Eur. J. Biochem. 250:354-363(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98180887; PubMed=9521588;
RA Lenkner U., Kestila M., Lamerdin J., McCreedy P., Adamson A.,
RA Olsen A., Tryggvason K.;
RT "Structure of the human amyloid-precursor-like protein gene APLP1 at
RT 19q13.1.";
RL Hum. Genet. 102:192-196(1998).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. C-TERMINALLY
CC PROCESSED IN THE GOLGI COMPLEX AND IS THEN SECRETED.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN, PARTICULARLY
CC IN THE CEREBRAL CORTEX POSTSYNAPTIC DENDRITY.
CC -1- PTM: N- AND O-GLYCOSYLATED.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U48437; AAB96331.1; -
DR EMBL; AD000864; AAB50173.1; -
DR HSSP; P05067; 1MMP.
DR MIT; 104775; -
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
KW Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 21
FT CHAIN 22 650
FT DOMAIN 22 580
FT TRANSMEM 581 603
FT DOMAIN 604 650
FT DOMAIN 640 643
FT DOMAIN 241 247
FT DOMAIN 264 268
FT CARBOHYD 337 337
FT N-LINKED (GLCNAC. . .) (POTENTIAL).

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DE Amyloid-like protein 1 precursor (APLP).
GN APLP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93066322; PubMed=1279693;
RA Masco W., Bupp K., Magendanz M., Gussella J.F., Tanzi R.E.,
RA Solomon F.;
RT "Identification of a mouse brain cDNA that encodes a protein related
to the Alzheimer disease-associated amyloid beta protein precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. MAY BE PROCESSED
CC IN THE GOLGI COMPLEX; HOWEVER, IT IS NOT YET CLEAR WHETHER APLP
CC IS SECRETED.
CC
CC -1 SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC
DR EMBL: L04538; AAA37247.1; .
DR PIR: A46362; A46362.
DR HSSP: P05067; IMWP.
DR MGD: MGI:88046; Apilp1.
DR InterPro: IPRO01868; A4_APP.
DR Pfam: PF02177; A4_EXTRA_1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA_1.
DR PROSITE: PS00319; A4_EXTRA_1.
DR PROSITE: PS00320; A4_INTRA_1.
DR Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 20
FT CHAIN 21 653
FT DOMAIN 21 583
FT TRANSHEM 584 606
FT DOMAIN 607 653
FT DOMAIN 643 646
FT DOMAIN 263 271
FT CARBOHYD 464 464
FT FT 554 554
SQ SEQUENCE 653 AA; 72751 MW; 5651DC3BA40EAB0 CRC64;

Query Match 28.4%; Score 1150.5; DB 1; Length 653;
Best local similarity 35.4%; Pred. No. 4.8e-53;
Matches 274; Conservative 120; Mismatches 228; Indels 153; Gaps 19;

QY	1	MLEGLALLLAAMTKARA-LEVPTDGNAGLAEPOIAFCGRLNHMHNVNQKMSDPSCGT	59
DB	22	LLP-TSLILLRQAQLAVGMLAVGPSAAEPASAOAYACGRLLTLHRDLRTGMEPPDORS	80
QY	60	KTCIDTFREGILOYCOEVPPELTQITNVVAVANDPVYTONCKRGKRCKCTKHNP-RVIPTCL	118
DB	81	RRCLLDPORVLEYECROMPELTHIKRWEDAQAATIPERWCGSTRSGRCAPHNIEVVEPHCL	140
QY	119	VGEFVSALLVTPDKCFKHQERMVNVCETHLMHTVAKECTSEKSTNLADYGMLPCGGIDK	178
DB	141	PGEVFSEALLVPECRCFLHQERMDCGSSTRRHQEAQCASSQGILLHGSMGLPCGGSDR	200
QY	179	FRCGVETCCPLAEESSDVNSADAEEODSDVR-WGGAQTDVADGSEDKVVEVAEEEEVAEV	237
DB	201	FRGVETVCCP-PPATPPPSGMAAGDPSTRSPVLGR-----AEGCD-----EEVESF	248
QY	238	EELFADDEDDEDDEVEEAEFEYEATEITTSIATTTTTTSVEVEVAEVCSEQAET	297
DB	249	PQPVDDTVFVEPPQAEEEEEEEERRAPPSSHP-----	281

QY 298 GPCRAMISRMWEDYEGKCAPFFYGGCGNNRNPDEEYCAVAGSAMSGSLKTTQEP 357
 DB 282 ---VMSR---VT----- 288
 QY 358 ARDPKLTPTASTDAVDKYLETPGDENENAHFOKAKERLEAKHREMSQVREWEAE 417
 DB 289 ---PPTPT-----DGVYVYGMPEIGEHEGFLRAKMDLEERMROQNEVREMANAD 339
 QY 418 ROAKLVPADKKAIVIOHQEKVESLEQANERQOLVETTHARVAMLNDRRRLALENTI 477
 DB 340 SQSKMLPKADRALNEHQSIQTLQEEVSGERQRLVETHTATRYTALINDORRALEGL 399
 QY 478 TALQAVPRPRHVRFMMLKKYVAERQKQHTLKEHEVRMVDKPKAAQIRSQVMTHLVI 537
 DB 400 AALQDPRQAEERLALRKRYLAEQKEQHTLRHYOHAADVPEKAAQIRFOVOTHLVI 459
 QY 538 YERNMOSLILYVPAVAEEIODEVELQEKONTSDVLANMISEPRISYGDALMP-S 596
 DB 460 EERNMOSGLLDONHNLAEQLOELL-----LAEHLQPSL---DASVFGS 505
 QY 537 LREITVYELLVNGEFSLDLQPMHSGADSVPAENTENEVEVDARPADRGITTRPGS 656
 DB 506 SSEDK-----GSLQ-----PESKDDPPYTLT---KGSTDOESS 536
 QY 657 GLTNKTEIEISVVKMDAEERHDSGYEVHH---QKLVFAEDVGSKKALIGLVAGVIA 713
 DB 537 SSGREKLTPLEDEYQKVNASAPRPFHSSDQRLDELAPSGTGVREALISGLLNGAGGG 596
 QY 714 TVIVITLVL--KKQOYTSIHNGVEVDAVTPPEERHLSKMOONGYENPTYKFEQ 767
 DB 597 SLIVLILLRKKKRYPTISHGVVEVDPMLTLEEQRLRELQNHGNGENPTYRLEE 651

RESULT 10

A4_DROME STANDARD: PRT; 886 AA.
 ID A4_DROME
 AC P14599:
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Beta-amyloid-like protein precursor.
 GN APPL OR VND.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCB1_TaxID=7227;
 N [1]
 RX MEDLINE=89184650; PubMed=2494667;
 RA Rosen D.R., Martin-Morris L., Luo L., White K.;
 RT "A Drosophila gene encoding a protein resembling the human
 RT beta-amyloid protein precursor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:2478-2482(1989).
 CC [2]
 CC SEQUENCE OF 1-83 FROM N.A.
 CC MEDLINE=91184006; PubMed=2127912;
 RA Martin-Morris L.E., White K.;
 RT "The Drosophila transcript encoded by the beta-amyloid protein
 RT precursor-like gene is restricted to the nervous system.";
 RL Development 110:185-195(1990)
 CC -1- FUNCTION: PROBABLY CORRESPONDS TO THE PROTEIN ENCODED BY THE
 CC ESSENTIAL LOCUS VND. A GENE REQUIRED FOR EMBRYONIC NERVOUS
 CC SYSTEM DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: APPL TRANSCRIPTS ARE FOUND IN THE CENTRAL AND
 CC PERIPHERAL NERVOUS SYSTEMS. WITHIN THE NERVOUS SYSTEM TRANSCRIPTS
 CC ARE NOT OBSERVED IN NEUROBLASTS, NEWLY GENERATED NEURONS AND AT
 CC LEAST ONE CLASS OF PRESUMED GLIAL CELLS.
 CC -1- DEVELOPMENTAL STAGE: APPL TRANSCRIPTS ARE FOUND IN POST-MITOTIC
 CC NEURONS IN THE CENTRAL AND PERIPHERAL NERVOUS SYSTEMS IN ALL
 CC DEVELOPMENTAL STAGES.

CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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 CC
 DR EMBL; J04516; AAA28874.1; -;
 DR EMBL; X55774; CAA39294.1; -;
 DR EMBL; X55775; CAA39294.1; JOINED.
 DR PTR: A32758; A32758.
 DR HSPSP; P05067; IMP.
 DR FLYBASE; FBgn0000108; Appl.
 DR InterPro; IPR001868; A4_APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW SIGNAL; Transmembrane; Amyloid; Neurogenesis.
 FT SIGNAL 1 27
 FT CHAIN 28 886
 FT DOMAIN 28 810
 FT TRANSMEM 811 833
 FT DONAIN 834 886
 FT DONAIN 876 879
 FT CARBOHYD 150 150
 FT CARBOHYD 161 161
 FT CARBOHYD 236 236
 FT CARBOHYD 239 239
 FT CARBOHYD 573 573
 SQ SEQUENCE 886 AA; 98261 MW; C5C1EA4194DB5A8D CRC64;

Query Match 18.2%; Score 737.5; DB 1; Length 886;
 Best Local Similarity 24.7%; Pred. No. 2.2e-31;
 Matches 235; Conservative 137; Mismatches 313; Indels 265; Gaps 30;

QY 7 LLLAAMTARLAEVPTDGNAGLLA-----EPOIAMFC--GRLLNMHNV-QNGKWDSDSG 58
 DB 9 LLLASLAWVLAI-----STAQVQASPRMPEQIAVLCAGQIYQPOLYSEEGRWYTDLSK 63
 QY 59 T---KTCTDTEKGIQYQGYEYVPELQINNVYEAQNPVITQWCKRG---RROCKTHPHFV 112
 DB 64 KTGPTCLRDMDLIDYCKAYPNMDITNVESSHQKIGGCRGALNAAACKSGSHRWI 123
 QY 113 IPRCLVGEFVSALLVPDKCFLLHQRMDVCETHLHHHTVAKETCSKSTLHDYGMIL 172
 DB 124 KPRCLT-GPQSDALVYEGCLFDHINASRCMPVRRNNGGAACQGRGMQRTFAMIL 182
 QY 173 PGIDKFRGVEVFCP-----LAESDQNV--SA 199
 DB 183 PGGISVFGSVFVCCPKHFKTDEIHVKRTDLPVMPAQINSANDELMDDEDSNDSYSK 242
 QY 200 DAEEDSDVMWGANPDVADGSEDKVVEVAEEV--AEV 237
 DB 243 DANEDDL-----DEDLMDGDEDDNVADPAATAGSPNTGSGSDNSGSLDINLEY 296
 QY 238 EE-EAADDDEDEDEVEEAEEPEYEA-TERTSIATTTTTTVEEYVREVCSDQA 295
 DB 297 DSGEGDNYEEDGAGSEEAEEVAMDSGAKVYSLKSDSSPSASAVYAPRAKAPKS 356
 QY 296 ETGPCRAMISRMWEDYEGKCAPFFYGGCGNNRNPDEEYCAVAGSAMSGSLKTTQOE 355
 DB 357 ESIVSTPOL-----ASAAAFVANSQSGT-----GAGAPPTSTAOPTSD 396
 QY 356 PLARPVVLTPTASTPAVDKYLETPGDENENAHFOKAKERLEAKHREMSQVREWE 415
 DB 397 P-----YTHEDPHYEHOSYKVSQRKLESHREKTVRKWDSD 435
 QY 416 AERQAKNLPKADKA-----VIOHQEKVESLEQANERQOLVETTHARVAMLNDRLDR 468

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Db 436 LBEKYODMLADPKAQSQRKQRTAFQTSVALLEEGNAEKHQLAMHQRYLAHINOR 495
Qy 469 RRLALENYITLQAAPPBRPHVFNMLKKYVRAEOKDRQHTLKFHEH-VAMVPD---KKA 524
Db 496 KREAMTCYQALTEQPPNNAHVEKCLKLRALHNRALAHYRLRLLSGSGPGGLEA 555
Qy 525 QIRSOVMHLRYVERMNSLSLVNPAVAEI-----ODEV----- 562
Db 556 SERPRTLERLIDIRAVNSMTLKRYPPLSAKIAQLMNDYILALSKDIDIGSLGME 615
Qy 563 -----DELQEQNTSDVLAN 579
Db 616 EAEAGLIDKYRVEIERKVAEKERLAEKORKEQRAAREKLEELRLAEKAVDMKLS 675
Qy 580 MISE-----PRISYNDALM-----PSLTKTKTVLLPVG 611
Db 676 QVAEQSOQPTOSQOAOQOQEKSLPKELGPDALVLTANPNLETKS----- 726
Qy 612 EFSLDDLOPMHSFGADSVANTENEVEVPDARPADRGLTTPRGSLTNKTEEISEVKM 671
Qy 727 EKDLSTSE---YGEATVSTKQGVLPVDDDAVQRAVEDVA---VAHQEA 773
Qy 672 DAEFRDSCYEYHOKLVF---PAEDVGSNK---GAIGLWGSVVAIVITVLWL 723
Db 774 EPOVQHFMTHDIGHRESSFLRREFQAQHAHAKEGRNVTFTLSFAGIALMAAFVGAV 833
Qy 724 KRKOYTSIH-HGVENVDAVTP-----EERHLSKMOQNGYENPTYKFE 766
Db 834 KRRTSRSPHAGGFIEVDQNVTHHPIVREKIVPNMQINGENPTYKYFE 883

RESULT 11
A4_MACFA STANDARD: PRT: 87 AA.
ID A4_MACFA P53601:
AC 01-OCT-1996 (Rel. 34, Created)
AC 30-MAY-2000 (Rel. 39, Last sequence update)
AC 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein (Fragment).
GN APP.
OS Macaca fascicularis (Crah eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9541;
RN [1]
RP MEDLINE=91273117; PubMed=1905108;
RT Podlisy M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
CC Am. J. Pathol. 138:1423-1435(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPPI/KUNITZ INHIBITOR DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M58726; AAA36828.1; -
DR HSSP: P05067; IAAP.

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DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BP1.
DR Pfam: PF00014; Kunitz_BP1.1.
DR PRINTS: PR00759; BASICPRASE.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4-EXTRA; PARTIAL.
DR PROSITE: PS00320; A4-INTRA; PARTIAL.
DR PROSITE: PS00280; BP1_KUNITZ_1; 1.
DR PROSITE: PS0279; BP1_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Alternative splicing;
KW Serine protease inhibitor.
FT NON_TER 1 79
FT DOMAIN 4 79
FT ACT_SITE 16 17
FT DISULFID 6 56
FT DISULFID 15 39
FT DISULFID 31 52
FT NON_TER 87 87
SQ SEQUENCE 87 AA; 9608 MW; B67C690DE0E0E7FF CRC64;

Query Match 11.3%; Score 457; DB 1; Length 87;
Best Local Similarity 95.4%; Pred. NO. 5.1e-18;
Matches 83; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 286 VREYCSQDAETGPCRAMISRWFEDVTEGKCAFPPYGGCGGRNNPDTEYCMAYCSAM 345
Db 1 VREYCSQDAETGPCRAMISRWFEDVTEGKCAFPPYGGCGGRNNPDTEYCMAYCSAM 60
Qy 346 SOSLKTTOEPLARDPVKLPPTAATP 372
Db 61 SOSLKTTRPLRDPVKLPPTAATP 87

RESULT 12
A4_MACNU STANDARD: PRT: 76 AA.
ID A4_MACNU P29216:
AC 01-DEC-1992 (Rel. 24, Created)
AC 01-DEC-1992 (Rel. 24, Last sequence update)
AC 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein (Fragment).
GN APP.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RP TISSUE=Brain;
RA Koo E.H., Sisodia S.S., Price D.L.;
RT Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPPI/KUNITZ INHIBITOR DOMAIN.
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CC -----
DR EMBL: X15985; CAA34116.1; -
DR PIR: S06678; S06678.
DR HSSP: P05067; ITAW.

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DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF000014; Kunitz_BPTI.1.
DR SMART: SM00131; KU.1.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
DR PROSITE: PS00280; BPTI_KUNITZ.1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ.2; 1.
KW Glycoprotein; Amyloid; Neurone; Alternative splicing;
KW Serine protease inhibitor.
FT NON_TER 1
FT DOMAIN 1 76 BPTI/KUNITZ INHIBITOR.
FT ACT_SITE 13 14 REACTIVE BOND.
FT DISULFID 3 53 BY SIMILARITY.
FT DISULFID 12 36 BY SIMILARITY.
FT DISULFID 28 49 BY SIMILARITY.
FT NON_TER 76 76
SQ SEQUENCE 76 AA: 8527 MW: 492BF3069AB082A1 CRC64;
Query Match 9.9%; Score 403; DB 1; Length 76;
Best Local Similarity 94.7%; Pred. No. 2.8e-15;
Matches 72; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 289 EVCSQAEFTGCPGRAMISRWYDVEGKCAPFEYGGCGGNRNFTDEYCMAYCGSAMSQS 348
DB 1 EVCSQAEFTGCPGRAMISRWYDVEGKCAPFEYGGCGGNRNFTDEYCMAYCGSAMSQS 60
QY 349 LKKTQEPPLARDPVKL 364
DB 61 LKKTREPLTRDPVKL 76
RESULT 13
A4_BOVIN
ID A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-NOV-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
DE APP.
GN Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
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CC -----
CC EMBL: X56124; CAA39589.1; -
CC EMBL: X56126; CAA39591.1; -
CC HSP: P05067; IBA4.

DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT NON_TER 59 59
SQ SEQUENCE 59 AA: 6414 MW: F43469D48BA2E12D CRC64;
Query Match 7.2%; Score 292; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 666 ISEVKMDAEPFRHDSGEVHHOKLVFPADVGSNKGAIIGLWGVATVITVLMKL 724
DB 1 ISEVKMDAEPFRHDSGEVHHOKLVFPADVGSNKGAIIGLWGVATVITVLMKL 59
RESULT 14
A4_RABIT
ID A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
DE APP.
GN Oryctolagus cuniculus (Rabbit).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC -----
CC EMBL: X56129; CAA39594.1; -
CC HSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
FT NON_TER 58 58
SQ SEQUENCE 58 AA: 6300 MW: F434209D8BBA82D CRC64;
Query Match 7.1%; Score 288; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 667 SEVKMDAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIAIVITVIMLK 724
DB 1 SEVKMDAEFRHDSGYEVHOKLVFAEDVGSNKGAIIGLMVGVVIAIVITVIMLK 58

RESULT 15

A4_SHEEP STANDARD: PRT: 58 AA.

AC 028757:

DI 01-NOV-1997 (Rel. 35, Created)

DI 01-NOV-1997 (Rel. 35, Last sequence update)

DI 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-Ap) (A-beta)] (Fragment).

DE APP.

GN Ovis aries (Sheep).

GN Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

GN Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

GN Bovidae; Caprinae; Ovis.

GN NCBI_TaxID=9940;

GN [1]

GN SEQUENCE FROM N.A.

GN TISSUE-Heart;

GN MEDLINE=92017079; PubMed=1656157;

GN Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

GN "Conservation of the sequence of the Alzheimer's disease amyloid

GN peptide in dog, polar bear and five other mammals by cross-species

GN polymerase chain reaction analysis.";

GN Brain Res. Mol. Brain Res. 10:299-305(1991).

GN -I- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO

GN INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN

GN G(O) (BY SIMILARITY).

GN -I- SUBCELLULAR LOCATION: Type I membrane protein.

GN -I- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -----

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CC -----

DR EMBL: X56130; CAA39595.1; -

DR HSSP: P05067; IAML.

DR InterPro: IPR001868; A4_APP.

DR PROSITE: PS00319; A4-EXTRA: PARTIAL.

DR PROSITE: PS00320; A4-INTRA: PARTIAL.

KW Glycoprotein; Amyloid; Neurone; Transmembrane.

FT CHAIN 1 1

FT DOMAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).

FT TRANSMEM 34 37 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 58 >58 POTENTIAL.

FT NON_TER 58 58 CYTOPLASMIC (POTENTIAL).

SO SEQUENCE 58 AA; 6300 MW; F434209D8EBA82D CRC64;

Query Match 7.1%; Score 288; DB 1; Length 58;

Best Local Similarity 100.0%; Pred. No. 2e-09;

Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: October 31, 2002, 10:12:24

Job time : 21.048 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:56 : Search time 48.3026 seconds
(without alignments)
2737.743 Million cell updates/sec

Title: US-09-785-215-2
Perfect score: 4058
Sequence: 1 MFGALLLLAAWTAFALEV.....KMQNGVNPNTYKFFEQMN 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPREMBL.19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_proteus:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_virus:*
17: sp_bacteriophage:*
18: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3981	98.1	770	09TU10	09tu10 sus scrofa
2	3719.5	91.7	13	09DGJ7	09dgj7 gallus gall
3	3590.5	88.5	6	09SKN7	09skn7 macaca fasc
4	3522.5	86.8	11	060496	060496 cavia sp. p
5	3489.5	86.0	695	11	P97487 mus musculu
6	3403.5	83.9	747	13	P91963 xenopus. ap
7	3377.5	83.2	695	13	09DGJ8 gallus gall
8	3163.5	78.0	693	13	098SG0 xenopus lae
9	3152.5	77.7	695	13	098SP9 xenopus lae
10	3065	75.5	607	11	099KJ2 mus musculu
11	2814	71.8	699	13	057394 narke japon
12	2831	69.8	547	4	013764 homo sapien
13	2785.5	68.6	738	13	090W28 brachydanio
14	2763.5	68.1	780	13	073683 tetraodon f
15	2717	67.0	569	13	09PVL1 gallus gall
16	2699	66.5	737	13	093279 fugu rudrip

17	2562.5	63.1	534	13	093296	093296 gallus gall
18	2446.5	56.3	484	4	013793	013793 homo sapien
19	2288.5	50.4	612	13	0919E7	0919E7 brachydanio
20	1960.5	48.3	763	11	061482	061482 mus musculu
21	1956.5	48.2	751	11	060709	060709 mus musculu
22	1733.5	42.7	695	4	013861	013861 homo sapien
23	1721	42.4	669	4	014662	014662 homo sapien
24	1709.5	42.1	695	11	064348	064348 mus musculu
25	1569	38.7	305	4	09BR38	09br38 homo sapien
26	1302	32.1	523	4	014594	014594 homo sapien
27	1267	31.2	522	4	09BR36	09br36 homo sapien
28	1159.5	28.6	650	4	096A92	096a92 homo sapien
29	788	19.4	160	11	090278	090278 cavia sp. p
30	786	19.4	684	5	0952X1	0952x1 caenorhabdi
31	784	19.3	680	5	010651	010651 caenorhabdi
32	739	18.2	887	5	09U4H3	09u4h3 drosophila
33	738	18.2	887	5	09TVV0	09tvv0 drosophila
34	678	16.7	136	6	P79307	P79307 sus scrofa
35	661	16.3	816	5	09W5F1	09w5f1 drosophila
36	561	13.8	182	11	09CYS4	09cys4 mus musculu
37	493	12.1	97	6	013778	013778 homo sapien
38	478	11.8	97	6	028673	028673 oryctolagus
39	411	10.1	82	4	P78438	P78438 homo sapien
40	402	9.9	75	4	09U058	09u058 homo sapien
41	393.5	9.7	82	4	016019	016019 homo sapien
42	389.5	9.6	82	4	016014	016014 homo sapien
43	387.5	9.5	82	4	016020	016020 homo sapien
44	376	9.3	79	11	035463	035463 cricetus
45	374	9.2	74	11	060495	060495 cavia sp. a

ALIGNMENTS

RESULT 1
ID 09TU10 PRELIMINARY: PRT: 770 AA.
AC 09TU10:
DT 01-MAY-2000 (TRMBLrel. 13, Created)
DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB032550; BAA84580.1; -.
DR HSSP: P05067; IAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR PRINTS: PR00759; BASICPTASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTR; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_2; 1.
DR Serine protease inhibitor.
SQ SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BC583E CRC64;
Query Match 98.1%; Score 3981; DB 6; Length 770;
Best Local Similarity 97.8%; Pred. No. 2.8e-240;
Matches 753; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
OY 1 MFGALLLLAAWTAFALEVPTDGNAGLLAEPOIAMFCGRILMHMNVONGKWDSPSGTK 60

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Db      1 MLPGALVLLAAMTARALEVPTDGNAGLLAEQVAMFCCKLMHNNVONGKWESEDPSTGK 60
Qy      61 TCIDTKEGILQCOEYVPELOITNVVEANQPTIOMNCKRGRKCKTHPHFVPIRYCLVG 120
Db      61 TCIDTKEGILQCOEYVPELOITNVVEANQPTIOMNCKRGRKCKTHPHFVPIRYCLVG 120
Qy      121 EFVSDALLVPDKCKFLHORMDVCEETHLHMHTVAKETSEKSTNLHDYGMILLPGSIDKFR 180
Db      121 EFVSDALLVPDKCKFLHORMDVCEETHLHMHTVAKETSEKSTNLHDYGMILLPGSIDKFR 180
Qy      181 GVEFVCCPLAEESDNDVSDAEEDSDVWVGADTDYADGSDKVVVEAEVEAEVEE 240
Db      181 GVEFVCCPLAEESDNDVSDAEEDSDVWVGADTDYADGSDKVVVEAEVEAEVEE 240
Qy      241 EADDEDEDEDEGEVEEAEPEYEATEERTSTATTTTTTESEVEVEVEVEVEVEVEVE 300
Db      241 EADDEDEDEDEGEVEEAEPEYEATEERTSTATTTTTTESEVEVEVEVEVEVEVEVE 300
Qy      301 RAMISRMVFDVTEGKCAPFEYGGCGGNRNNDTEEYCAVCGSAMSOSILKTQBPCLARD 360
Db      301 RAMISRMVFDVTEGKCAPFEYGGCGGNRNNDTEEYCAVCGSAMSOSILKTQBPCLARD 360
Qy      361 PVKLTPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
Db      361 PVKLTPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
Qy      421 KNLPRADKRAVIOHFOEYVESLEOEANERQOLVETHMARVAMLNDRRRLALENYITL 480
Db      421 KNLPRADKRAVIOHFOEYVESLEOEANERQOLVETHMARVAMLNDRRRLALENYITL 480
Qy      481 QAVPRPRHVFEMLKYYRAEQRDROHTLKHEHVRMVDPKKAAQIRSOVMTHLVIER 540
Db      481 QAVPRPRHVFEMLKYYRAEQRDROHTLKHEHVRMVDPKKAAQIRSOVMTHLVIER 540
Qy      541 MNOSLSLYNPAVAEEIODEVDELLOKEQNSDDVLANMISEPRISYGNALMPSLET 600
Db      541 MNOSLSLYNPAVAEEIODEVDELLOKEQNSDDVLANMISEPRISYGNALMPSLET 600
Qy      601 KTTVELLPVNGEFLDDLOPMHSPGADSVPAANTEVEVEVPDARPAADGLTTRPGSLTN 660
Db      601 KTTVELLPVNGEFLDDLOPMHSPGADSVPAANTEVEVEVPDARPAADGLTTRPGSLTN 660
Qy      661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLVGVAIVATVITL 720
Db      661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLVGVAIVATVITL 720
Qy      721 VMLKKQYTSIHGVEVDAVTPREHLSKMOQNGYENPTYKFFEQMON 770
Db      721 VMLKKQYTSIHGVEVDAVTPREHLSKMOQNGYENPTYKFFEQMON 770
Qy      721 VMLKKQYTSIHGVEVDAVTPREHLSKMOQNGYENPTYKFFEQMON 770
Db      721 VMLKKQYTSIHGVEVDAVTPREHLSKMOQNGYENPTYKFFEQMON 770

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RESULT 2

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ID      09D6J7      PRELIMINARY;      PRT;      751 AA.
AC      09D6J7;
DT      01-MAR-2001 (TREMUREL. 16, Created)
DT      01-MAR-2001 (TREMUREL. 16, Last sequence update)
DT      01-DEC-2001 (TREMUREL. 19, Last annotation update)
DE      BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Sarasu M., Rodolosse A., Sorribas V.;
RT      "Cloning of full-length chicken beta-amyloid precursor protein
RT      isoforms."
RL      Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF289219; AAC00594.1; -.
DR      HSSP; P05067; 1BA4.

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DR      InterPro: IPR001868; A4_APP.
DR      InterPro: IPR002223; Kunitz_BPTI.
DR      Pfam: PF02177; A4_EXTRA; 1.
DR      Pfam: PF00014; Kunitz_BPTI; 1.
DR      PRINTS: PR00203; AMYLOIDA.
DR      PRINTS: PR00759; BASICPTASE.
DR      SMART: SM00006; A4_EXTRA; 1.
DR      SMART: SM00131; KU; 1.
DR      PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR      PROSITE: PS50279; BPTI_KUNITZ_2; 1.
KW      Serine protease inhibitor.
SQ      SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

```

Query Match 91.7%; Score 3719.5; DB 13; Length 751;
 Best Local Similarity 91.7%; Pred. No. 5.6e-224;
 Matches 708; Conservative 18; Mismatches 23; Indels 23; Gaps 4;

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Qy      1 MLPGALVLLAAMTARALEVPTDGNAGLLAEQVAMFCCKLMHNNVONGKWESEDPSTGK 60
Db      1 MLPHALLLLAAGARALEVPADGAGLLAEPOIAMFCCKLMHNNVONGKWESEDPSTGK 60
Qy      61 TCIDTKEGILQCOEYVPELOITNVVEANQPTIOMNCKRGRKCKTHPHFVPIRYCLVG 120
Db      61 TCIDTKEGILQCOEYVPELOITNVVEANQPTIOMNCKRGRKCKTHPHFVPIRYCLVG 120
Qy      121 EFVSDALLVPDKCKFLHORMDVCEETHLHMHTVAKETSEKSTNLHDYGMILLPGSIDKFR 180
Db      121 EFVSDALLVPDKCKFLHORMDVCEETHLHMHTVAKETSEKSTNLHDYGMILLPGSIDKFR 180
Qy      181 GVEFVCCPLAEESDNDVSDAEEDSDVWVGADTDYADGSDKVVVEAEVEAEVEE 240
Db      181 GVEFVCCPLAEESDNDVSDAEEDSDVWVGADTDYADGSDKVVVEAEVEAEVEE 240
Qy      241 EADDEDEDEDEGEVEEAEPEYEATEERTSTATTTTTTESEVEVEVEVEVEVEVEVE 300
Db      241 EADDEDEDEDEGEVEEAEPEYEATEERTSTATTTTTTESEVEVEVEVEVEVEVEVE 300
Qy      301 RAMISRMVFDVTEGKCAPFEYGGCGGNRNNDTEEYCAVCGSAMSOSILKTQBPCLARD 360
Db      301 RAMISRMVFDVTEGKCAPFEYGGCGGNRNNDTEEYCAVCGSAMSOSILKTQBPCLARD 360
Qy      361 PVKLTPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
Db      361 PVKLTPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREWEAEARQA 420
Qy      421 KNLPRADKRAVIOHFOEYVESLEOEANERQOLVETHMARVAMLNDRRRLALENYITL 480
Db      421 KNLPRADKRAVIOHFOEYVESLEOEANERQOLVETHMARVAMLNDRRRLALENYITL 480
Qy      481 QAVPRPRHVFEMLKYYRAEQRDROHTLKHEHVRMVDPKKAAQIRSOVMTHLVIER 540
Db      481 QAVPRPRHVFEMLKYYRAEQRDROHTLKHEHVRMVDPKKAAQIRSOVMTHLVIER 540
Qy      541 MNOSLSLYNPAVAEEIODEVDELLOKEQNSDDVLANMISEPRISYGNALMPSLET 600
Db      541 MNOSLSLYNPAVAEEIODEVDELLOKEQNSDDVLANMISEPRISYGNALMPSLET 600
Qy      601 KTTVELLPVNGEFLDDLOPMHSPGADSVPAANTEVEVEVPDARPAADGLTTRPGSLTN 660
Db      601 KTTVELLPVNGEFLDDLOPMHSPGADSVPAANTEVEVEVPDARPAADGLTTRPGSLTN 660
Qy      661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLVGVAIVATVITL 720
Db      661 IKTEEISEVKMDAEFRHDSGYEVHOKLVFAEDVGSNKGAIIIGLVGVAIVATVITL 720
Qy      721 VMLKKQYTSIHGVEVDAVTPREHLSKMOQNGYENPTYKFFEQMON 770
Db      721 VMLKKQYTSIHGVEVDAVTPREHLSKMOQNGYENPTYKFFEQMON 770
Qy      721 VMLKKQYTSIHGVEVDAVTPREHLSKMOQNGYENPTYKFFEQMON 770
Db      721 VMLKKQYTSIHGVEVDAVTPREHLSKMOQNGYENPTYKFFEQMON 770

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RESULT 3

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ID      095KN7      PRELIMINARY;      PRT;      695 AA.

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AC 095KN7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crib eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N. A.
RC TISSUE=CEREBELLUM;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlinsky M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
RR EMBL: M58727; AAA36829.1; -.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 597 636 POTENTIAL.
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 88.5%; Score 3590.5; DB 6; Length 695;
Best Local Similarity 90.1%; Pred. No. 5.6e-216;
Matches 694; Conservative 1; Mismatches 0; Indels 75; Gaps 1;

QY 1 MHPGIALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLMHNHNVNGKWDSPSGTK 60
DB 1 MHPGIALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLMHNHNVNGKWDSPSGTK 60
QY 61 TCIDRKEGILQYCEQVYPELQITNVNVEANQPTIQNMCKRGKCKKTHHFVIPPCLVG 120
DB 61 TCIDRKEGILQYCEQVYPELQITNVNVEANQPTIQNMCKRGKCKKTHHFVIPPCLVG 120
QY 121 EFVSALLVLPDKCKFLHQRMDVCEHLHMTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSALLVLPDKCKFLHQRMDVCEHLHMTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
QY 121 EFVSALLVLPDKCKFLHQRMDVCEHLHMTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSALLVLPDKCKFLHQRMDVCEHLHMTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFYCCPLAEESDNDVSDADAEDSDVWVGADTDYADGSEDKVVEVAEEVEEVAEVEE 240
DB 181 GVEFYCCPLAEESDNDVSDADAEDSDVWVGADTDYADGSEDKVVEVAEEVEEVAEVEE 240
QY 241 EADDDEDEDGDEVEEAEDEPEEATERTSTATTTTTTSEVEEVEVVCSEQAETGFC 300
DB 241 EADDDEDEDGDEVEEAEDEPEEATERTSTATTTTTTSEVEEVEVVCSEQAETGFC 300
QY 241 EADDDEDEDGDEVEEAEDEPEEATERTSTATTTTTTSEVEEVEVVCSEQAETGFC 300
DB 241 EADDDEDEDGDEVEEAEDEPEEATERTSTATTTTTTSEVEEVEVVCSEQAETGFC 300
QY 301 RAMISRWFVDYEGKCAFFYGGCGGNRNPNFTEEYCAVCSANSQSLLKTTQEPRLARD 360
DB 301 RAMISRWFVDYEGKCAFFYGGCGGNRNPNFTEEYCAVCSANSQSLLKTTQEPRLARD 360
QY 289 ----- 288
QY 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREMEAEERQA 420
DB 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREMEAEERQA 420
QY 289 ---VPTTAASPDADVADKYLETPGDENEHAHFQAKERLEAKHREMSQVMREMEAEERQA 345
DB 289 ---VPTTAASPDADVADKYLETPGDENEHAHFQAKERLEAKHREMSQVMREMEAEERQA 345
QY 421 KNLPRADKKAIVIQHFOEKVESLEQEAANRQOLVETNHARVAMNDRRRLALENTYIAL 480
DB 421 KNLPRADKKAIVIQHFOEKVESLEQEAANRQOLVETNHARVAMNDRRRLALENTYIAL 480
QY 346 KNLPRADKKAIVIQHFOEKVESLEQEAANRQOLVETNHARVAMNDRRRLALENTYIAL 405
DB 346 KNLPRADKKAIVIQHFOEKVESLEQEAANRQOLVETNHARVAMNDRRRLALENTYIAL 405
QY 481 QAVPRPRHVFNMLKKYVAEQKROHNLKHFENHVMVDPKKAQAIQSVQMTLHVIYER 540
DB 481 QAVPRPRHVFNMLKKYVAEQKROHNLKHFENHVMVDPKKAQAIQSVQMTLHVIYER 540
QY 406 QAVPRPRHVFNMLKKYVAEQKROHNLKHFENHVMVDPKKAQAIQSVQMTLHVIYER 465
DB 406 QAVPRPRHVFNMLKKYVAEQKROHNLKHFENHVMVDPKKAQAIQSVQMTLHVIYER 465
QY 541 KNOGSLILYNPVAVEIDEVDELQEQNTSDVLANMISEPRISTGNDALMPSLTET 600
DB 541 KNOGSLILYNPVAVEIDEVDELQEQNTSDVLANMISEPRISTGNDALMPSLTET 600
QY 466 KNOGSLILYNPVAVEIDEVDELQEQNTSDVLANMISEPRISTGNDALMPSLTET 525
DB 466 KNOGSLILYNPVAVEIDEVDELQEQNTSDVLANMISEPRISTGNDALMPSLTET 525
QY 601 KTTVELLPVNGEFSLDDLOPMHSFGADSVPAENTENVEVEVDARPAADRGLTTRPSSGLN 660
DB 601 KTTVELLPVNGEFSLDDLOPMHSFGADSVPAENTENVEVEVDARPAADRGLTTRPSSGLN 660
QY 526 KTTVELLPVNGEFSLDDLOPMHSFGADSVPAENTENVEVEVDARPAADRGLTTRPSSGLN 585
DB 526 KTTVELLPVNGEFSLDDLOPMHSFGADSVPAENTENVEVEVDARPAADRGLTTRPSSGLN 585
QY 661 KTEEISEVKMDAEFRHDSGVEVNHQKLVFAEDVGSNKGALIGLMVGCVIATVITL 720
DB 661 KTEEISEVKMDAEFRHDSGVEVNHQKLVFAEDVGSNKGALIGLMVGCVIATVITL 720

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DB 586 KTEEISEVKMDAEFRHDSGVEVNHQKLVFAEDVGSNKGALIGLMVGCVIATVITL 645
QY 721 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOONGENPYTKFPEQMON 770
DB 646 VMLKKQYTSIHGVEVDAVTPPEERHLSKMOONGENPYTKFPEQMON 695

RESULT 4
ID 060496 PRELIMINARY; PRT; 695 AA.
AC 060496;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N. A.
RC TISSUE=BRAIN;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL: X97631; CA66230.1; -.
DR HSSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 86.8%; Score 3522.5; DB 11; Length 695;
Best Local Similarity 88.2%; Pred. No. 9.8e-212;
Matches 679; Conservative 7; Mismatches 9; Indels 75; Gaps 1;

QY 1 MHPGIALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLMHNHNVNGKWDSPSGTK 60
DB 1 MHPGIALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRLMHNHNVNGKWDSPSGTK 60
QY 61 TCIDRKEGILQYCEQVYPELQITNVNVEANQPTIQNMCKRGKCKKTHHFVIPPCLVG 120
DB 61 TCIDRKEGILQYCEQVYPELQITNVNVEANQPTIQNMCKRGKCKKTHHFVIPPCLVG 120
QY 121 EFVSALLVLPDKCKFLHQRMDVCEHLHMTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSALLVLPDKCKFLHQRMDVCEHLHMTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
QY 121 EFVSALLVLPDKCKFLHQRMDVCEHLHMTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
DB 121 EFVSALLVLPDKCKFLHQRMDVCEHLHMTVAKETSEKSTNLHDYGMLLPCGIDKFR 180
QY 181 GVEFYCCPLAEESDNDVSDADAEDSDVWVGADTDYADGSEDKVVEVAEEVEEVAEVEE 240
DB 181 GVEFYCCPLAEESDNDVSDADAEDSDVWVGADTDYADGSEDKVVEVAEEVEEVAEVEE 240
QY 241 EADDDEDEDGDEVEEAEDEPEEATERTSTATTTTTTSEVEEVEVVCSEQAETGFC 300
DB 241 EADDDEDEDGDEVEEAEDEPEEATERTSTATTTTTTSEVEEVEVVCSEQAETGFC 300
QY 241 EADDDEDEDGDEVEEAEDEPEEATERTSTATTTTTTSEVEEVEVVCSEQAETGFC 300
DB 241 EADDDEDEDGDEVEEAEDEPEEATERTSTATTTTTTSEVEEVEVVCSEQAETGFC 300
QY 301 RAMISRWFVDYEGKCAFFYGGCGGNRNPNFTEEYCAVCSANSQSLLKTTQEPRLARD 360
DB 301 RAMISRWFVDYEGKCAFFYGGCGGNRNPNFTEEYCAVCSANSQSLLKTTQEPRLARD 360
QY 289 ----- 288
QY 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREMEAEERQA 420
DB 361 PVKLPPTAASPDAVDKYLETPGDENEHAHFQAKERLEAKHREMSQVMREMEAEERQA 420
QY 289 ---VPTTAASPDADVADKYLETPGDENEHAHFQAKERLEAKHREMSQVMREMEAEERQA 345
DB 289 ---VPTTAASPDADVADKYLETPGDENEHAHFQAKERLEAKHREMSQVMREMEAEERQA 345
QY 421 KNLPRADKKAIVIQHFOEKVESLEQEAANRQOLVETNHARVAMNDRRRLALENTYIAL 480
DB 421 KNLPRADKKAIVIQHFOEKVESLEQEAANRQOLVETNHARVAMNDRRRLALENTYIAL 480
QY 346 KNLPRADKKAIVIQHFOEKVESLEQEAANRQOLVETNHARVAMNDRRRLALENTYIAL 405
DB 346 KNLPRADKKAIVIQHFOEKVESLEQEAANRQOLVETNHARVAMNDRRRLALENTYIAL 405

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QY 481 QAVPRPRHVFNMKKYVAEOKDRQHTLKHEHVRMVDPKKAAQIRSOVMTHLRIYER 540
DB 406 QAVPRPRHVFNMKKYVAEOKDRQHTLKHEHVRMVDPKKAAQIRSOVMTHLRIYER 465
QY 541 MNOSLSLYNPAVAEEIODEVDLQKQONSSDVLAMNISEPRISYNDALMPSLTET 600
DB 466 MNOSLSLYNPAVAEEIODEVDLQKQONSSDVLAMNISEPRISYNDALMPSLTET 525
QY 601 KTTVELLPNGEESLDDLPWHSFGADSVPAANTENEVEVDARPADRLTTRPGSGLTN 660
DB 526 KTTVELLPNGEESLDDLPWHSFGADSVPAANTENEVEVDARPADRLTTRPGSGLTN 585
QY 661 KTEEISEVKMDAEFRHDSGYEVNHOKLVFPAEDVGSNKGAIIGLWGVVATVITL 720
DB 586 KTEEISEVKMDAEFRHDSGYEVNHOKLVFPAEDVGSNKGAIIGLWGVVATVITL 645
QY 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMQONGYENPTYKFEOMON 770
DB 646 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMQONGYENPTYKFEOMON 695

RESULT 5
P97487 PRELIMINARY: PRT: 695 AA.
ID P97487; P97487;
AC P97487; P97487;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HIPOCAMPAL AMYLOID PROTEIN.
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAMP8; TISSUE=HIPPOCAMPUS;
RA Flood J.F., Kumar V.B., Sasser T., Morley J.E.;
RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 581-662 FROM N.A.
RC STRAIN=1295V;
RA Wragg M.A., Busfield F., Duff K., Korenbiat K., Capechi M.,
RA Loring J.F., Goate A.M.;
RL Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
DB EMBL: U84012; AAB41502.1;
DB HSSP: P05067; IMMP.
DB MGI: 88059; APP.
DB InterPro: IPR001868; A4_APP.
DB Pfam: PF02177; A4_EXTRA; 1.
DB PRINTS: PR00203; AMYLOID4.
DB SMART: SM00006; A4_EXTRA; 1.
DB PROSITE: PS00319; A4_EXTRA; 1.
DB PROSITE: PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA: 78414 MW: 9A5FBEZED261236E CRC64:

Query Match 86.0%; Score 3489.5; DB 11; Length 695;
Best Local Similarity 87.7%; Pred. No. 1.1e-209;
Matches 675; Conservative 6; Mismatches 14; Indels 75; Gaps 1;

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QY 181 GVEFVCCPLAEESDNVDADAEEDSDVMWGGADTDYADGSEDKYVEVAEEVEAE 240
DB 181 GVEFVCCPLAEESDSVDSDADAEEDSDVMWGGADTDYADGSEDKYVEVAEEVEAE 240
QY 241 EADDEDEDEDEGEVEEAEPPEATERTSTATTTTTEVEVEVRVCSQEAETGCG 300
DB 241 EADDEDEDEDEGEVEEAEPPEATERTSTATTTTTEVEVEVRVCSQEAETGCG 288
QY 301 RAMISRWFVDVTEGCAPEFTYGGCGNNRNPDTBEYCAVCSAMSQSILKTTQEPLARD 360
DB 289 ----- 288
QY 361 PVKLTPTASTPDADVDTLETGPDENENAHFQAKERLEAKHREMSOVMREMEAE 420
DB 289 ---VPTTASTPDADVDTLETGPDENENAHFQAKERLEAKHREMSOVMREMEAE 345
QY 421 KNLPRADKKAVIOHQEKEVSELOEANEQOLVETNHARVAMLNDRRRLALENTAL 480
DB 346 KNLPRADKKAVIOHQEKEVSELOEANEQOLVETNHARVAMLNDRRRLALENTAL 405
QY 481 QAVPRPRHVFNMKKYVAEOKDRQHTLKHEHVRMVDPKKAAQIRSOVMTHLRIYER 540
DB 406 QAVPRPRHVFNMKKYVAEOKDRQHTLKHEHVRMVDPKKAAQIRSOVMTHLRIYER 465
QY 541 MNOSLSLYNPAVAEEIODEVDLQKQONSSDVLAMNISEPRISYNDALMPSLTET 600
DB 466 MNOSLSLYNPAVAEEIODEVDLQKQONSSDVLAMNISEPRISYNDALMPSLTET 525
QY 601 KTTVELLPNGEESLDDLPWHSFGADSVPAANTENEVEVDARPADRLTTRPGSGLTN 660
DB 526 KTTVELLPNGEESLDDLPWHSFGADSVPAANTENEVEVDARPADRLTTRPGSGLTN 585
QY 661 KTEEISEVKMDAEFRHDSGYEVNHOKLVFPAEDVGSNKGAIIGLWGVVATVITL 720
DB 586 KTEEISEVKMDAEFRHDSGYEVNHOKLVFPAEDVGSNKGAIIGLWGVVATVITL 645
QY 721 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMQONGYENPTYKFEOMON 770
DB 646 VMLKKQYTSIHGVEVDAAVTPPEERHLSKMQONGYENPTYKFEOMON 695

RESULT 6
Q91963 PRELIMINARY: PRT: 747 AA.
ID Q91963;
AC Q91963;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE development regulation of the human beta-amyloid precursor protein;
GN APP747.
GN APP747.
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae.
OX NCBI_Taxid=8353;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-93129227; PubMed-1282805;
RA Okada H., Okamoto H.;
RL "A Xenopus homologue of the human beta-amyloid precursor protein:
RL development regulation of its gene expression.";
DB Biochem. Biophys. Res. Commun. 189:1561-1568 (1992).
DB EMBL: S52417; AAB24853.1;
DB HSSP: P05067; IH23.
DB InterPro: IPR001868; A4_APP.
DB Pfam: PF02177; A4_EXTRA; 1.
DB Pfam: PF00014; Kunitz_BPTI. 1.
DB PRINTS: PR00203; AMYLOID4.
DB PRINTS: PR00759; BASICPTASE.
DB SMART: SM00006; A4_EXTRA; 1.
DB SMART: SM00131; KU; 1.

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DB 644 TLVMLKKQYTSIHGVEVDAATPTEERHLTKMQONGYENTYKFEQMON 695

RESULT 8

Q98SG0 PRELIMINARY; PRT; 693 AA.

DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE BETA-AMYLOID PRECURSOR PROTEIN A.
 GN APP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCBL_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RS Van den Hurk W.H.;
 RS Thesis (2001), Department of Biological Sciences,
 RS University of Nijmegen, Nijmegen, Netherlands.
 DR EMBL; AJ298150; CAC37193.1;
 DR HSP; P05067; I423.
 DR InterPro; IPR001868; A4_APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Signal.
 FT SIGNAL 1 18 POTENTIAL.
 SQ SEQUENCE 693 AA; 78568 MW; CAFIDF655CIAB653 CRC64;

Query Match 78.0%; Score 3163.5; DB 13; Length 693;
 Best Local Similarity 79.1%; Pred. No. 2.5e-189;
 Matches 611; Conservative 37; Mismatches 43; Indels 81; Gaps 5;

QY 1 MLPGIALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRILMNMNVONGKWDSPSGTK 60
 DB 1 MLPHITLLVTV-GALALEVPADNGSLAEPOIAMFCGRILMNMNVONGKWDSPSGTK 59
 QY 61 TCIDTKEGIILOCOEYVPELOITNVVEANOPVTIONMCKRGRKCKKTPHPIVRYCLVG 120
 DB 60 GCIGTKEGIILOCOEYVPELOITNVVEANOPVTIONMCKRGRKCKKTPHPIVRYCLVG 119
 QY 121 EFVSADALLVPDKCKFLHOERMDVCEHLMHTVAKETSEKSTNLMHDYGMILPGIDKFR 180
 DB 120 EFVSADALLVPDKCKFLHOERMDVCEHLMHTVAKETSEKSTNLMHDYGMILPGIDKFR 179
 QY 181 GVEFVCCPLAEESDNDVSDAEDSDVWVGADTDYADGSEDKVVEVA--EEEEVAEVE 238
 DB 180 GVEFVCCPLAEESDNDVSDAEDSDVWVGADTDYADGSEDKVVEVA--EEEEVAEVE 238
 QY 239 EEEADDEDDDDGDEVEEAEPEPEATEERTSTATTTTTTTESEVEEVVRCVSEQAETG 298
 DB 239 EEEADDEDDDDGDEVEEAEPEPEATEERTSTATTTTTTTESEVEEVVRCVSEQAETG 298
 QY 299 PCRAMISWYTDVTEGKCAPFFYGGCGGNRPDTEECMAVCGSAMOSILKTTQEPILA 358
 DB 287 ----- 286
 QY 359 RDPVKLPPTASTPDVAVKYLETPGDENEHNAFOKAKERLEAKHREKRSQVREMEAEER 418
 DB 287 -----VPTASTPDVAVKYLETPGDENEHNAFOKAKERLEAKHREKRSQVREMEAEER 418
 QY 419 QAKNLPRADKAIVIOHFOEKVESLEOEANERQOLVETHTMAVEMALNDRRLALENYIT 478
 DB 342 QAKNLPRADKAIVIOHFOEKVESLEOEANERQOLVETHTMAVEMALNDRRLALENYIT 401
 QY 479 ALQAVPRPRVFNMLKKYVBAEQKROHTLKHPEHVMNDPCKRAAQIRSQVNMHLRYIY 538
 DB 402 ALQAVPRPRVFNMLKKYVBAEQKROHTLKHPEHVMNDPCKRAAQIRSQVNMHLRYIY 461

RESULT 9

Q98SF9 PRELIMINARY; PRT; 695 AA.

DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE BETA-AMYLOID PRECURSOR PROTEIN B.
 GN APP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NC NCBL_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RS Van den Hurk W.H.;
 RS Thesis (2001), Department of Biological Sciences,
 RS University of Nijmegen, Nijmegen, Netherlands.
 DR EMBL; AJ298151; CAC37194.1;
 DR HSP; P05067; I423.
 DR InterPro; IPR001868; A4_APP.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 KW Signal.
 FT SIGNAL 1 18 POTENTIAL.
 SQ SEQUENCE 695 AA; 78803 MW; DCI4EB02AFB0204A CRC64;

Query Match 77.7%; Score 3152.5; DB 13; Length 695;
 Best Local Similarity 78.9%; Pred. No. 1.2e-188;
 Matches 609; Conservative 39; Mismatches 45; Indels 79; Gaps 5;

QY 1 MLPGIALLLLAAMTARALEVPTDGNAGLLAEPOIAMFCGRILMNMNVONGKWDSPSGTK 60
 DB 1 MLPHITLLVTV-GALALEVPADNGSLAEPOIAMFCGRILMNMNVONGKWDSPSGTK 59
 QY 61 TCIDTKEGIILOCOEYVPELOITNVVEANOPVTIONMCKRGRKCKKTPHPIVRYCLVG 120
 DB 60 GCIGTKEGIILOCOEYVPELOITNVVEANOPVTIONMCKRGRKCKKTPHPIVRYCLVG 119
 QY 121 EFVSADALLVPDKCKFLHOERMDVCEHLMHTVAKETSEKSTNLMHDYGMILPGIDKFR 180
 DB 120 EFVSADALLVPDKCKFLHOERMDVCEHLMHTVAKETSEKSTNLMHDYGMILPGIDKFR 179
 QY 181 GVEFVCCPLAEESDNDVSDAEDSDVWVGADTDYADGSEDKVVEV--AEEVEVAEVE 238
 DB 180 GVEFVCCPLAEESDNDVSDAEDSDVWVGADTDYADGSEDKVVEV--AEEVEVAEVE 238
 QY 239 EEEADDEDDDDGDEVEEAEPEPEATEERTSTATTTTTTTESEVEEVVRCVSEQAETG 298
 DB 239 EEEADDD-DEDDGDETEEPEPEATEERTSTATTTTTTTESEVEEVVRAV----- 289

OS Unidentified.
 XX
 PN WO200052048-A1.
 XX
 PD 08-SEP-2000.
 XX
 PF 03-MAR-2000; 2000WO-US05574.
 XX
 PR 04-MAR-1999; 99US-0122736.
 XX
 PA (PRAE-) PRAECIS PHARM INC.
 XX
 PI Findeis MA, Phillips K, Olson GL, Self C;
 XX
 DR WPI; 2000-594168/56.
 XX
 PT Novel compounds that are useful as modulators of beta-amyloid peptide
 aggregation in treating amyloidosis, comprises D-amino acids
 XX
 CC Disclosure: Page 9; 87pp; English.
 CC
 CC The present sequence is beta-amyloid peptide. The present invention
 relates to peptides (see AAB27023-B27046) that modulate beta-amyloid
 peptide aggregation, and hence inhibit the neurotoxicity of beta-amyloid
 peptide. The beta-amyloid peptide modulators would be useful for
 CC treating disorders associated with beta-amyloidosis for e.g. Alzheimer's
 CC disease. The present sequence is derived from amyloid precursor protein
 CC via proteolysis. The gene for amyloid precursor protein maps to
 CC chromosome 21.
 CC
 SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 21; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGVIAT 43
 DB 1 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGVIAT 43

RESULT 14
 AAB15372
 ID AAB15372 standard; peptide; 43 AA.
 XX
 AC AAB15372;
 XX
 TT 17-JAN-2001 (first entry)
 XX
 CC Human beta-amyloid precursor protein A-beta fragment.
 XX
 KM Human; beta-amyloid precursor protein; beta-APP; Alzheimer's disease;
 KM chromosome 21; epitope.
 XX
 OS Homo sapiens.
 XX
 PN WO200042166-A2.
 XX
 PD 20-JUL-2000.
 XX
 PF 13-JAN-2000; 2000WO-US00872.
 XX
 PR 13-JAN-1999; 99US-0115749.
 XX
 PA (DUPO) DUPONT PHARM CO.
 XX
 PI Selfert DA, Mitchell TJ;
 XX
 DR WPI; 2000-476049/41.
 XX
 PT A cDNA construct that encodes beta-amyloid precursor protein for
 identifying compounds which inhibit A-beta peptide release and/or
 PT synthesis comprises an epitope tag within the A-beta sequence -

XX
 PS Disclosure: Page 13-14; 42pp; English.
 XX
 CC The present sequence is A-beta fragment of the human beta-amyloid
 CC precursor protein (beta-APP). It was used in the production of peptides
 CC of the invention. The invention concerns the production, detection and
 CC characterisation of epitope-tagged beta-APP proteins, and their use in
 CC identifying modulators of beta-APP which can be used to treat diseases
 CC associated with an altered metabolism of the protein, in particular
 CC Alzheimer's disease.
 CC
 SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 21; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGVIAT 43
 DB 1 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGVIAT 43

RESULT 15
 AAB21216
 ID AAB21216 standard; peptide; 43 AA.
 XX
 AC AAB21216;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Beta-amyloid peptide.
 XX

KW Beta-amyloid peptide; membrane-spanning glycoprotein; analgesic;
 KW nicotinic agonist; beta-amyloid precursor protein; APP;
 KW Alzheimer's disease.
 XX

OS Homo sapiens.
 XX
 PN US6117901-A.
 XX
 PD 12-SEP-2000.
 XX
 PF 21-NOV-1997; 97US-0976179.
 XX
 PR 22-NOV-1996; 96US-0098551.
 XX

XX (ATHE-) ATHENA NEUROSCIENCES INC.
 PA (ELIL) LILLY & CO ELI.
 XX

PI Thorsett ED, Nissen JS, Wu J, Latimer LH, John V, Fang LY;
 PI Audia JE, Mabry TE;
 XX
 DR WPI; 2000-637551/61.
 XX

PT Eliciting analgesic effect in mammal, e.g. human, involves
 administering an aryl substituted olefinic amine compound -
 XX
 PS Disclosure: Column 11; 32pp; English.
 XX

CC The present sequence is the beta-amyloid peptide, which is part of
 CC a large membrane-spanning glycoprotein, referred to as the beta-amyloid
 CC precursor protein (APP). Aryl substituted olefinic amine (metanilcotline)
 CC compounds which inhibit beta-amyloid peptide release and/or its
 CC synthesis may be useful for treating Alzheimer's disease, both
 CC prophylactically and therapeutically.
 CC
 SQ Sequence 43 AA;

Query Match 100.0%; Score 222; DB 21; Length 43;
 Best Local Similarity 100.0%; Pred. No. 1.6e-25;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DAEFRHDSGYEVHOKLVFEADVGSNKGAIIGLMVGVIAT 43

|||||
Db 1 DAERHDSGEVHHOKLVFAEDVGSNKGALIGLWGVVIAT 43

Search completed: October 31, 2002, 10:12:01
Job time : 5.01476 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 31, 2002, 10:10:56 : Search time 2.69742 Seconds
(without alignments)
2757.743 Million cell updates/sec

Title: US-09-785-215-2_COPY-672-714

Perfect score: 222

Sequence: 1 DAFFRHDSGEVHHKQLVFF.....VGSNKATIGLMGVVIAT 43

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	222	100.0	82	4	P78438
2	222	100.0	82	4	Q16014
3	222	100.0	82	4	Q16019
4	222	100.0	82	4	Q16020
5	222	100.0	534	13	Q93296
6	222	100.0	695	6	Q95KN7
7	222	100.0	695	11	Q60496
8	222	100.0	695	13	Q9D6J8
9	222	100.0	751	13	Q9D6J7
10	222	100.0	770	6	Q9TUI0
11	217	97.7	569	13	Q9PVL1
12	212	95.5	97	4	Q13778
13	203	91.4	79	11	Q35463
14	203	91.4	607	11	Q9PK32
15	203	91.4	693	13	Q98SG0
16	203	91.4	693	13	P97487

17	203	91.4	747	13	Q91963
18	200	90.1	695	13	Q98SF9
19	193	86.9	699	13	O57394
20	180	81.1	780	13	O73683
21	176	79.3	33	4	Q9UC33
22	162.5	73.2	737	13	Q93229
23	162.5	73.2	612	13	Q919E7
24	162.5	73.2	738	13	Q90W28
25	162	73.0	30	4	Q9UCA9
26	147	66.2	28	4	Q9UCD1
27	126	56.8	49	6	O97917
28	106	47.7	19	4	Q9UCB8
29	64	28.8	20	4	Q9UCB6
30	64	28.8	328	2	Q9RPS4
31	64	28.8	755	2	Q9RPS4
32	64	28.8	755	2	Q9R717
33	64	28.8	755	2	Q9R472
34	62	27.9	755	2	Q44388
35	61	27.5	755	2	Q9WMA1
36	57.5	25.9	895	10	Q9AMB6
37	57	25.7	195	10	O22662
38	57	25.7	332	12	Q9DON5
39	57	25.7	365	12	Q9W055
40	57	25.7	575	10	O81120
41	55.5	25.0	678	16	O84344
42	55	24.8	291	16	O97T23
43	55	24.8	738	16	O92VFI
44	54.5	24.5	678	16	O9PK54
45	54.5	24.5	829	10	O9XGTO

ALIGNMENTS

RESULT 1	P78438	PRELIMINARY;	PRT;	82 AA.
ID	P78438			
AC	P78438			
DT	01-MAY-1997 (TREMBLrel. 03, Created)			
DT	01-MAY-1997 (TREMBLrel. 03, Last sequence update)			
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)			
DE	AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).			
GN	APP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89392030; PubMed=2675837;			
RX	MEDLINE=87120329; PubMed=2949367;			
RX	Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,			
RA	Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;			
RT	"Amyloid beta protein gene: cDNA, mRNA distribution, and genetic			
RT	linkage near the Alzheimer locus.";			
RL	Science 235:880-884(1987).			
RN	[3]			
RP	SEQUENCE OF 32-63 FROM N.A.			
RX	MEDLINE=9305397; PubMed=145269;			
RA	Kamito K., Orr H.T., Payami H., Witsman E.M., Alonso M.E., Pulst S.M.,			
RA	Anderson L., O'dahl S., Nemens E., White J.A.;			
RT	"Linkage and mutational analysis of familial Alzheimer disease			
RT	kinds for the APP gene region.";			
RL	Am. J. Hum. Genet. 51:998-1014(1992).			
DR	EMBL; M29270; AAA51768.1; -			
DR	EMBL; M29269; AAA51768.1; JOINED.			

DR EMBL; M15532; AAA51564.1; -
DR EMBL; S45136; AAB23646.1; -
DR HSSP; P05067; IBA4.
FT NON_TER 1
SO SEQUENCE 82 AA; 899 MW; 8DA9EA2B813A070E CRC64;
Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMGCVIAT 43
17 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMGCVIAT 59
RESULT 2
ID Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014; 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE BETA-AMYL0ID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor."
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; AAB26264.2; -
DR HSSP; P05067; IBA4.
FT NON_TER 1
FT NON_TER 82
Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMGCVIAT 43
18 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMGCVIAT 60
RESULT 3
ID Q16019 PRELIMINARY; PRT; 82 AA.
AC Q16019; 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE BETA-AMYL0ID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor."
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; AAB26264.2; -
DR HSSP; P05067; IBA4.
FT NON_TER 1
FT NON_TER 82

SO SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;
Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMGCVIAT 43
18 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMGCVIAT 60
RESULT 4
ID Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020; 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE BETA-AMYL0ID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Denman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor."
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61383; AAB26265.2; -
DR HSSP; P05067; IBA4.
FT NON_TER 1
FT NON_TER 82
SO SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;
Query Match 100.0%; Score 222; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMGCVIAT 43
18 DAEFRHDSGYEVHHQKLVFAEDVGSNKGAIIGLMGCVIAT 60
RESULT 5
ID Q93296 PRELIMINARY; PRT; 534 AA.
AC Q93296; 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE AMYL0ID PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
substrate for caspase-3 in dying motoneurons."
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -
DR HSSP; P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR PRINTS; PR00203; AMYL0ID4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.

FT NON_TER 1
SO SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 100.0%; Score 222; DB 13; Length 534;
Best Local Similarity 100.0%; Pred. No. 1e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAFFRHDSGYEVHHOKLVFAEDVGSNKGATIGLWVGVIAT 43
DB 436 DAFFRHDSGYEVHHOKLVFAEDVGSNKGATIGLWVGVIAT 478

RESULT 6

095KN7 PRELIMINARY; PRT; 695 AA.

AC 095KN7
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RX MEDLINE=91273117; PubMed=1905108;
RA Podlasy M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease";
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL; M58727; AAA36829.1; -
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 597 636
SQ SEQUENCE 695 AA; 78663 MW; 4FE6A0139F69D56 CRC64;

Query Match 100.0%; Score 222; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAFFRHDSGYEVHHOKLVFAEDVGSNKGATIGLWVGVIAT 43
DB 597 DAFFRHDSGYEVHHOKLVFAEDVGSNKGATIGLWVGVIAT 639

RESULT 7

060496 PRELIMINARY; PRT; 695 AA.

AC 060496
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=97236426; PubMed=9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CA66230.1; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.

DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_EXTRA; 1.
SO SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 100.0%; Score 222; DB 11; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAFFRHDSGYEVHHOKLVFAEDVGSNKGATIGLWVGVIAT 43
DB 597 DAFFRHDSGYEVHHOKLVFAEDVGSNKGATIGLWVGVIAT 639

RESULT 8

09DGJ8 PRELIMINARY; PRT; 695 AA.

AC 09DGJ8
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolose A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289218; AAG00593.1; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 100.0%; Score 222; DB 13; Length 695;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DAFFRHDSGYEVHHOKLVFAEDVGSNKGATIGLWVGVIAT 43
DB 597 DAFFRHDSGYEVHHOKLVFAEDVGSNKGATIGLWVGVIAT 639

RESULT 9

09DGJ7 PRELIMINARY; PRT; 751 AA.

AC 09DGJ7
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 751 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolose A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289219; AAG00594.1; -
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.

DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PRO0203; AMYLOIDA4.
DR PRINTS: PRO0759; BASICTPASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR Serine protease inhibitor.
SO SEQUENCE 751 AA; 84705 MW; E78E9413A8033D84 CRC64;

Query Match 100.0%; Score 222; DB 13; Length 751;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVIAT 43
DB 653 DAERHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVIAT 695
|||||

SOULT 10
09TU10
ID 09TU10 PRELIMINARY; PRT; 770 AA.
AC 09TU10;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE AMYLOID PRECURSOR PROTEIN.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura A., Takahashi T.;
RT "Amyloid Precursor Protein 770."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB032550; BAA84580.1; -
DR HSSP: P05067; IAA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS: PRO0203; AMYLOIDA4.
DR PRINTS: PRO0759; BASICTPASE.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS50279; BPTI_KUNITZ_2; 1.
DR Serine protease inhibitor.
SO SEQUENCE 770 AA; 86961 MW; 5F7A1DCB2BC583E CRC64;

Query Match 100.0%; Score 222; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVIAT 43
DB 672 DAERHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVIAT 714
|||||

RESULT 11
09PVL1
ID 09PVL1 PRELIMINARY; PRT; 569 AA.
AC 09PVL1;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN App.

OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Archaeosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN.
RA Coulson E.J., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family tells us about its function."
RL Neurochem. Int. 0:0-0(2000).
DR EMBL: AF030341; AAF12698.1; -
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PRO0203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SO SEQUENCE 569 AA; 64753 MW; 0AB8B851863A19D CRC64;

Query Match 97.7%; Score 217; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 4.9e-20;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAERHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVIAT 42
DB 472 DAERHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVIAT 513
|||||

RESULT 12
013778
ID 013778 PRELIMINARY; PRT; 97 AA.
AC 013778;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=67120326; Pubmed=3810169;
RA Goldgaber D., Lerman M.I., McBride O.W., Safiotti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding brain amyloid of Alzheimer's disease."
RL Science 235:877-880(1987).
DR EMBL: M15533; AAA3540.1; -
DR HSSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR PRINTS: PRO0203; AMYLOIDA4.
FT NON_TER 1
SO SEQUENCE 97 AA; 10884 MW; E528CDBA448DE474E CRC64;

Query Match 95.5%; Score 212; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 2.9e-20;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EFRHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVIAT 43
DB 1 EFRHDSGEVHHOKLVFAEDVGSNKGAIIGLMVGVIAT 41
|||||

RESULT 13
035463
ID 035463 PRELIMINARY; PRT; 79 AA.
AC 035463;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)

DT 01-DEC-2001 (TREMBLE). 19, last annotation update)
DE ALZHEIMER'S AMYLOID BETA PROTEIN (FRAGMENT).
CN BETA APP.
OS *Cricetulus griseus* (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC *Cricetulus*.
OX NCBI_TaxID-10029;
RN [1]
RP SEQUENCE FROM N.A.
RA Sambamurti K., Plinix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF030413; AAAB6608.1; -
DR HSSP; P05067; IBA4.
FT NON TER 1
FT 79
FT 79
SO SEQUENCE 79 AA; 8538 MW; 37F2C6C3BF3F557 CRC64;

Query Match	91.48%	Score 203;	DB 11;	Length 79;
Best Local Similarity	93.0%	Pred. No.	3,4e-19;	
Matches 40;	Conservative	1;	Mismatches 2;	Indels 0;
				Gaps 0;

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QY      1 DAEFRHDSGEVHHOKLVEFAEDVGSNKGAIIGLMVGGVIAAT   43  
        ||| |||| : ||| | | | | | | | | | | | | | |  
Db     21 DAEFGHDSGFEVRHQKLVEFAEDVGSNKGAIIGLMVGGVIAAT   63
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RESULT 14
Q99K32

DT 01-JUN-2001 (TREMBLrel. 17, created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE HYPOTHEITICAL 68.4 KDA PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Crniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;

RC TISSUE: MAMMARY TUMOR. MAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC TISSUE: .
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005490; AH05490.1; -.
DR HSSP; P05067; IAA.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPT1.
DR Pfam; PF000014; Kunitz_BPT1; 1.
DR PRINTS; PR002023; AMYLOIDA4.
DR PRINTS; PR007959; BASICPRASE.
DR SMART; SMO0131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPT1_KUNITZ_1; 1.
DR PROSITE; PS00279; BPT1_KUNITZ_2; 1.
KW Hypothetical protein, Serine protease inhibitor.
FT NON_TER 1
SQ SEQUENCE 607 AA; 68391 MW; BF802214CEA7D172 CRC64;

Query Match	91.4%	Score 203	DB 11	Length 607
Best Local Similarity	93.0%	Pred. No. 3.6e-16		
Matches 40; Conservative	1	Mismatches 2	Indels 0	Gaps 0

Oy 1 DAEFRHDSGEYEVHHOKLVFFAEDVGSNKGAIIGLMVGGVIAT 43
 |||| |::|:| | | | | | | | | | | | | | | | | |
Db 509 DAEFGHDSGEYEVRRHQKLVFAEDVGSNKGAIIGLMVGGVIAT 551

RESULT 15
Q98SGO PRELIMINARY; PRT; 693 AA
ID Q98SGO

AC		098SGJ-2001 (Tremblrel. 17, Created)	
DT	01-JUN-2001	(Tremblrel. 17, last sequence update)	
DT	01-JUN-2001	(Tremblrel. 17, last sequence update)	
DT	01-DEC-2001	(Tremblrel. 19, last annotation update)	
DE	BETA-AMYLOID PRECURSOR PROTEIN A.		
CN	APP.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_Taxid=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Van den Hurk W.H.;		
RL	Thesis (2001), Department of Biological Sciences,		
RL	University of Nijmegen, Nijmegen, Netherlands.		
DR	EMBL; AJ288150; CAC37193.1; -.		
DR	HSSP; P05067; IH23.		
DR	InterPro; IPR001868; A4_APP.		
DR	Pfam; PF02177; A4_EXTRA; 1.		
DR	PRINTS; PR00203; AMYLOIDA4.		
DR	SMART; SMO0006; A4_EXTRA; 1.		
DR	PROSITE; PS00319; A4_EXTRA; 1.		
DR	PROSITE; PS00320; A4_INTRA; 1.		
KW	Signal.		
FT	SIGNAL		
SEQ	SEQUENCE	693 AA; 78568 MW; CAFIDF65CIAB653 CRC64;	
		1	18
			POTENTIAL.
Query Match		91.4%; Score 203; DB 13; Length 693;	
Best Local Similarity		88.4%; Pred. No. 4.Le-18;	
Matches	38; Conservative	4; Mismatches	1;
		Indels	0; Gaps
			0;

QY 1 DAEFRHDSGYEVHHQKLVFAEDVGSNGKAIIIGLMVGVIAT 43
 |::|::|: |||||:|||||:|||||:|||||:|||||:|||||
Dd 595 DSEYRHDTAYEVHHQKLVEFAEVDGSGNKGAIIGLMVGGVIAT 637

Search completed: October 31, 2002, 10:14:35
Job time : 4.69742 secs

